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Yu, Misook

From:

Mosher, Marv

Sent:

Tuesday, August 19, 2003 7:22 AM

To: Subject: Yu, Misook RE: 09765086

Your judgement is better than mine in deciding whether or not there really is motivation to put the peices together, since you have read the references and I have not. If you, in your scientist role, sat down with the references, would it have occurred to you to put them together to get the invention, if you did not already know about the invention? If the invention is not a method of cancer treatment, is there an enablement issue on how to use the claimed invention for purposes other than treating cancer?

Sorry for the socratic response, but I really can't substitute my ignorance for your judgement. MM

----Original Message-----

From:

Yu, Misook

Sent:

Monday, August 18, 2003 12:38 PM

To:

Mosher, Mary

Subject:

09765086

There are 3 sets of method claims using a chimeric construct consisting of two parts (one, prostate-targeting peptide and the other, lyis-causing anti-microbial peptide).

The first set of claim says "a method of directing an antimicrobial peptide in vivo to prostate tissue";

The second set of claims says "a method of inducing apoptosis in prostate tissue in vivo"; and

The third set of claims says "a method of selectively inducing apoptosis in normal prostate tissue"

The first and second sets were rejected by combination of primary reference showing prostate-targeting peptides are known in the art to direct cancer treating agents to prostate, by two types of secondary reference showing that there is a need in the prostate cancer treatment art for a method to reduce generalized side effects, and antimicrobial peptide has been used for cancer treatment. Combination of the primary and secondary references teach all necessary components of the products for directing something to prostate or inducing apoptosis in prostate.

In reply to OA, applicant argues that their invention is not drawn to method of cancer treatment and there is no motivation why one in ordinary skill would be motivated to do the purpose specified in the preamble of the claims. The most of the specification is about prostate cancer treatment using the chimeric product. Do I drop the rejection?

Examiner Misook Yu, Ph.D. 703-308-2454 (Phone) Art Unit 1642 CM1-8E18 (Room) CM1-8E12 (Mail Box)

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Claim

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                                                                           The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
                                                                                                                                                                                                                                       Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or tissue, for i
                                     isolated in the present invention, antimicrobial peptide to make the
                                                                                                                                                                                                               Claim 25; Page
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                                                   prostate cancer or melanoma. The present sequence is a homing peptide isolated in the present invention, which can be conjugated to an
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                                                                                                                         The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively. Internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is mouse prostate homing peptide. This sequence is useful in the homing of pro-apoptotic
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ALIGNMENTS

RESULT AAY48905

AAY48905 standard; Peptide; 7

Membrane dipeptidase-binding prostate homing peptide #21

AAY48905; 10-DEC-1999

(first entry)

KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; XX Synthetic.

OS Synthetic.
OS Homo-sapiens

XX Homo-sap

Best Local Similarity 100.0%; Pred. No. 0.0029;

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                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                           LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy Compatible
COMPUTER: FLOPC COMPATIBLE
COMPUTER: FLOPC COMPATIBLE
COMPUTER: FLOPC COMPATIBLE
COMPOTER FLORE
COMPOTER FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILLING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Amphipathic Peptides NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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STREET: P. O. Box 2471
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 504 387-3221
TELEFAX: 504 346-8049
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                                                             Application US/08944133
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Pred. No. 0.0042;
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; MOLECULE TYPE: US-08-944-133-7
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Best Local Similarity
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/78
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Becker, Calvin L

TITLE OF INVENTION: Amphipathic Peptides

TITLE OF GEOMENCES: 54
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STRANDENNESS: sing)
TOPOLOGY
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CORRESPONDENCE ADDRESS:
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FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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P. O. Box 2471
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Pred. No. 0.0042;
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Copyright (c) 1993 - 2000 Comp
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US-08-94-1041-28
US-07-908-455A-62
US-08-45-1041-28
US-08-45-325-86
US-08-55-486-46
US-08-55-486-46
US-08-55-486-46
US-08-55-486-46
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US-09-340-154-46
US-09-335-40
PCT-US95-04335-40
PCT-US95-09338-45
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US-08-944-133-6
                                    ; MOLECULE TYPE: US-08-944-133-6
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GENERAL INFORMATION:
  Query Match
                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
TELEFAX: 504 346-8049
                                                                                                                                                              APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File
                                                                                                                                                                                                                                                           CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
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APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-0CT-1997
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipat
NUMBER OF SEQUENCES: 54
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                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 70821-2471
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STREET: P. O. Box 2471
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US-07-908-455A-64
US-08-434-120-30
US-08-434-120-90
US-08-465-325-30
US-08-465-325-88
US-08-2317-30A-24
US-08-427-001C-24
US-08-457-798-24
US-08-457-171-24
US-08-689-489C-24
US-08-689-489C-24
US-08-801-028-24
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PCT-US96-10041-23
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Ouzounis C.A., Georgatos S.D.;
"Bovine filensin possesses primary
to intermediate filament proteins."
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                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLULAR LOCATION: MEMBRANE - AND CYTOSKELETON - ASSOCIATED
-- TISSUE SPECIFICITY: LENS.
-- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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Viruses; dsDNA viruses, no RNA stage;
NCBI_TaxID=10506;
                                                                             between the Swiss Institute of Bioinf
the European Bioinformatics Institute
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Mammalia; Eutheria;
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  non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib
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462 AA; 52541 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND PARTIAL SEQUENCE
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                                                                                                                                                              TO THE INTERMEDIATE FILAMENT FAMILY.
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Pred. No.
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PROTEIN 1).
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Phycodnaviridae; Phycodnavirus
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27;
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330-kb genome: map
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RESULT 5
TOP1_DAUCA
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Matches
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Daucus carota (Carrot).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                                                                         TOP1_DAUCA P93119;
                                                                                                                 expression analysis in relation to cell proliferation.";
Gene 183:183-190(1996).
-I- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
-I- CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED
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REPEAT
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DOMAIN
               WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

-!- SIMILARITY: BELONGS TO THE EUKARYOTIC TYPE I TOPOISOMERASE FAMILY.
                                                                                                                                                                                   Carbonera D.;
                                                                                                                                                                                                     STRAIN=CV. LUNGA DI AMSTERDAM;
MEDLINE=97149297; PubMed=8996105;
                                                                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
DNA TOPOISOMERASE I (EC 5.99.1.2).
                                                                                                                                                          "Cloning of a cDNA encoding DNA topoisomerase I in Daucus expression analysis in relation to cell proliferation.";
                                                                                                                                                                                          Balestrazzi A.,
                                                                                                                                                                                                                            SEQUENCE FROM
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                                                DNA, FOLLOWED BY PASSAGE AND REJOINING.

MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.

MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBOODS, IT SIMULTANEOUSLY FORMS A PROTEIN DNA LINK, IN
                                                                                                                                                                                                                                                                                                                                                                                                                           GGKISKAFEKLGKMIK 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                           Toscano I., Bernacchia G., Luo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1664; IF
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TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
COIL 2.
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Pred. No.
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82;
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RESULT 6
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01-OCT-1996
20-AUG-2001
                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                           Defeo-Jones D., Huang P.S., Jones R.E.,
Hanobik M.G., Huber H.E., Oliff A.;
"Cloning of cDNAs for cellular proteins
retinoblastoma gene product.";
Nature 352:251-254(1991).
                                                                                                                                                                                                                                                                                              RBP2."
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0416; EUTPISMRASEI.
SMART; SM00435; TOPBUG; 1.
PROSITE; PS00176; TOPOISOMERASE_I_EUK; 1.
ISOMErase; Topoisomerase; DNA-binding.
ACT_SITE 749 749 DNA CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mendel; 17369; Dauca; 2787; 17369.
Mendel; 17369; Dauca; 2787; 17369.
InterPro; IPR001631; Topismerse_I.
Pfam; PF01028; Topoisomerase_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                 Oncogene
                                                                                                                                                                                                                                                                                                                        MEDLINE=94020841; PubMed=8414517; Fattaey A.R., Helin K., Dembski M.S., Dyson N., Vuocolo G.A., Hanobik M.G., Haskell K.M., Oliff Jones R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RBB2_HUMAN P29375;
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                                                                                                                                                                                                                                            MEDLINE=91312450; PubMed=1857421;
                                                                                                                                                                                                                                                                                                          "Characterization of the retinoblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RETINOBLASTOMA
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                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                             SUBCELLULAR LOCATION: NUCLEAR SIMILARITY: TO THE C-TERMINAL THE JUMONJI PROTEIN.
                                                                                                                                                    FUNCTION: INTERACTS WITH THE RETINOBLASTOMA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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5 (Rel. 34, La
6 (Rel. 40, La
7 (MA BINDING )
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34, Last sequence update)
40, Last annotation update)
NDING PROTEIN 2 (RBBP-2).
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Pred. No.
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DOMAIN OF TH
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                                                                                                                            XE169
                                                                                                                                                                                                                                                                                                          proteins RBP1
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A., Defeo-Jones
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Interpro: IPR001965; PHD.
Pfam; PF01388; ARID; 1.
Pfam; PF02373; JmjV; 1.
Pfam; PF02375; JmjV; 1.
Pfam; PF00628; PHD; 3.
SMART; SM00501; BRIGHT; 1.
SMART; SM00545; JmjV; 1.
R SMART; SM00545; JmjV; 1.
18 SMART; SM00545; JmjV; 1.
18 SMART; SM00545; JmjV; 1.
19 SMART; SM00545; JmjV; 1.
19 SMART; SM00545; JmjV; 1.
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01-NOV-1990
01-FEB-1996
CHLOROPLAST
                                                                                                                                                                                                     MEDLINE-95395841; pubMed-7666415;
Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
"Complete sequence of the maize chloroplast genome:
hotspots of divergence and fine tuning of genetic in
transcript editing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RK2_MAIZE
P17788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1552
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                                                                                                                                                                                J. Mol.
[3]
                                                                                                                                                                                                                                                                                                Kavousi M., Giese K., Larrinua I.M., Subramanian A.R.; "Nucleotide sequence and map positions of the duplicat maize (Zea mays) chloroplast ribosomal protein L2."; Nucleic Acids Res. 18:4244-4244(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM;
                                                                                                            Hoch B., Maier R.M., Appel K., "Editing of a chloroplast mRNA Nature 353:178-180(1991).
                                                                                                                                                    RNA EDITING OF INITIATOR CODON. mEDLINE=91367263; Pubmed=1653905;
                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90332419;
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    Panicoideae; Andropogoneae;
NCBI_TaxID=4577;
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InterPro; IPR003349;
InterPro; IPR001965;
          modified
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                                                                              SIMILARITY: BELONGS TO THE L2P FAMILY OF CAUTION: THE INITIATOR METHIONINE IS CREA
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1722 AA;
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nilarity 90.98;
Conservative
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         -profit institution this statement is
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JmjN.
PHD.
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          Usage
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EMBL; X65563; CAA60329.1; I
EMBL; X65563; CAA60371.1;
EMBL; X62070; CAA43983.1; I
PIR; S10500; R5ZM2.
PIR; S17874; S17874.
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pfam; pF00181; Ribosomal_L2; 1.
pR0SITE; pS00467; RIBOSOMAL_L2; 1.
Ribosomal protein; Chloroplast; RNA editing.
SEQUENCE 273 AA; 30065 MW; BA65197231EA3CAO CRC64;
                                                                                                               This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us entitles requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SINGLE-STRANDED DNA BINDING PROTEIN (HELIX-DESTABILIZING
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINB-89016637; PubMed-3262868;

McPheeters D.S., Stormo G.D., Gosch G., Gold I

McPheeters D.S., Stormo f.D., Gosch G., Gold I

"Nucleotide sequences of the bacteriophage T2

Nucleic Acids Res. 16:9341-9342(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, T4-like phages.
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01-NOV-1988
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                                                          EMBL; X12460; CAA3100
EMBL; X12460; CAA3100
PIR; S01437; DDBP32.
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32 OR SSB.
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                                                                                                                                                                                                                                                          FUNCTION: BINDS PREFERENTIALLY TO SINGLE-STRANDED THEREFORE, DESTABLLIZES DOUBLE-STRANDED DNA. IT IS REPLICATION, REPAIR AND RECOMBINATION. BINDS SS-DN REPLICATION FORK ADVANCES AND STIMULATES THE REPLIP PROCESSIVITY AND ACCURACY.
SUBUNIT: HOMODIMER IN THE ABSENCE OF DNA, MONOMER
                                                                                                                                                                                                                     MISCELLANEOUS: INTERACTS WITH THE POLYMERASE AND THE UVSX AND UVSY PROTEINS (BY SIMILARITY).
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                                                                          CAA31000.1;
CAA31001.1;
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Pred. No.
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P03695; 1GPC

DNA-binding;

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replication;

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Zinc. 65 78 DNA repair;

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P09797;
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89016637, pubMed=3262868;
McPheeters D.S., Stormo G.D., Gosch G., Gold L.;
"Nucleotide sequences of the bacteriophage T2 and T6
Nucleic Acids Res. 16:9341-9342(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SINGLE-STRANDED DNA BINDING PROTEIN (HELIX-DESTABILIZING
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NCBI_TaxID=10666;
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MISCELLANEOUS: INTERACTS WITH THE POLYMERASE AND
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MGTAAMGGAAATAAKKADKVA 260
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78 88 88
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ID DNAK_M
AC Q9ZFC6
DT 20-AUG
DT 20-AUG

DNAK_METSS

STANDARD;

PRT;

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Q9ZFC6; 20-AUG-2001 20-AUG-2001

(Rel. 40, Created)
(Rel. 40, Last sequence update)

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RESULT 10
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01-NOV-1995
01-FEB-1996
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InterPro; IPR001384;
InterPro; IPR000130;
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-i- PTM: PROBABLY POSSESSES THREE DISULFIDE BONDS.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M35 (ZINC
METALLOPROTEASE); ALSO KNOWN AS THE DEUTEROLYSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: THERMOSTABLE METALLOPROTEASE. SHOWS HIGH ACTIVITIES ON BASIC NUCLEAR SUBSTRATES SUCH AS HISTONE AND PROTAMINE.
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF BONDS WITH HYDROPHOBIC RESIDUES IN P1'; ALSO 3-ASN-|-GLN-4 AND 8-GLN-|-SER-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91360097; PubMed=1886621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NEUTRAL PROTEASE II PRECURSOR (EC 3.4.24.39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPII_ASPOR
P46076;
                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00768; DEUTEROLYSIN.
PROSITE; PS00142; ZINC_PROTEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S53810; AAB19701.1; -.
                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000130; Zn_MTpeptdse
Pfam; PF02102; Peptidase_M35; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5062;
                                                             159
                                                                                                      œ
                                                             GGKAAKVTKALSQLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BONDS IN INSULIN B CHAIN.
                                                                                                      GGKLAKLAKKLAKLAK 23
                                                                                                                                             Similarity 50.08; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Metalloprotease;
                                                                                                                                                                                                                                                      Ā
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352
303
304
307
37517
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                                                                                                                                                                 40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptidase_M35
                                                             174
                                                                                                                                                                                                                                                                                                                                                                                  PROTEASE; 1.

protection; signal;
                                                                                                                                                                                                                                                      WW;
                                                                                                                                             Score 42; DB
Pred. No. 57;
4; Mismatches
                                                                                                                                                                                                                                                                     NEUTRAL PROTEASE II.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                      070C5131335B7F44 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352
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                                                                                                                                                                                                                                                                                                                                                                                               Zymogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEUTEROLYSIN) (NPII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eurotiomycetes,
                                                                                                                                               4;
                                                                                                                                                                                    Length 352;
                                                                                                                                                                                                                                                                                                                 SIMILARITY).
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Best Local
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                                                                                                                                                                                                                                                                    P08956;
01-NOV-1988 (Rel. 09, Created)
01-FEB-1995 (Rel. 31, Last seque
20-AUG-2001 (Rel. 40, Last annot
TYPE I RESTRICTION ENZYME ECOKI
HSDR OR HSR OR B4350.
                                                                                                                                                                                                                                                                                                                                                                            ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

EDOM C.Y., Kim Y.M.;

"grpE, dhaK, and dhaJ genes of Methylovorus sp. strain SS1 DSM11726."

"grpE, dhaK, and dhaJ genes of Methylovorus sp. strain SS1 DSM11726."

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).

-I- FUNCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, So
Blattner F.R.;
                                                                                                                 "Organization K-12.";
                                                                                                                                                                                                                               Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methylovorus sp. (strain Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. CHAPERONE PROTEIN (HSP70).
                                                                                                   J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chaperone;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00012; HSP70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P04475; 2BPR.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF106835; AAC95378.1; -. HSSP; P04475; 2BPR.
                                                                                                                                            Loenen W.A.M., Daniel A.S.,
                                                                                                                                                           MEDLINE=88118919;    PubMed=3323532;
                                                                                                                                                                           STRAIN=K1
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                T1RK_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=81683;
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                                                                                                    Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity
9; Conser
                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-binding; Heat shock. 641 AA; 69764 MW; 7DFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                    198:159-170(1987)
                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40, Last annotation update)
DNAK (HEAT SHOCK PROTEIN 70) (HEAT SHOCK 70 KDA
                                                                                                                          niel A.S., Braymer H.D.,
sequence of the hsd gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.48;
                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
ZYME ECOKI R PROTEIN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS1 / DSM 11726).
; beta subdivision; Methylophilus
                                                                                                                                                                                                                                              gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB Pred. No. 98;
                               Sofia H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7DFA5EBE144825CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                       cion update)
PROTEIN (EC
                                                                                                                               genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                            Murray N.E.;
                               Daniels
                                                                                                                                of Escherichia
                                                                                                                                                                                                                                              Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ن</u>
                                                                                                                                                                                                                                                                                      3.1.21.3) (R.ECOKI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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PPOC_TOBAC
ID PPOC_T
AC 024163
DT 15-DEC
DT 15-JUL
DE PROTOP
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Best Local S
Matches 11
                                                     PPOC_TO: 024163;
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Nucleic Acids
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restriction system.";
J. Bacteriol. 173:5207-5219(1991).
-i- FUNCTION: THE ECOKI ENZYME RECOGNIZES 5'AACN(6)GTGC-3'. SUBUNIT--i- FUNCTION: THE ECOKI ENZYME RECOGNIZES ACTIVITIES, BUT NOT FOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X06545; CAA29791.1; ALT_FRAME. EMBL; U14003; AAA97247.1; -. EMBL; AE000505; AAC77306.1; -. EMBL; X54198; CAA38116.1; ALT_INIT. PIR; Q00648; NDECKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1999 (Rel. 38, Last annotation update)
PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00271; helicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Benner J.S.;
"Characterization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-27 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                       Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91317743;
                                                                                                                                                                                                                                                                                                                                                                    Restriction system; Hydrolase; DNA-binding; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EcoGene; EG10459; hsdR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REBASE; 980;
                                                                                                                                     216
                                                                                                                                                               υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MODIFICATION.

SUBUNIT: THE TYPE I RESTRICTION/MODIFICATION SYSTEM IS COMPOSED OF THREE POLYPEPTIDES R,M AND S.

OF THREE POLYPEPTIDES R,M AND S.

MISCELLANEOUS: TYPE I RESTRICTION AND MODIFICATION ENZYMES ARE COMPLEX, MULTIFUNCTIONAL SYSTEMS WHICH REQUIRE ATP, S-ADENOSYL METHIONINE AND MG(2+) AS CO-FACTORS AND, IN ADDITION TO THEIR ENDONUCLEOLYTIC AND METHYLASE ACTIVITIES, ARE POTENT DNA-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: REF 1 SEQUENCE DIFFERS FROM THAT SHOWN FROM CNWARD AND IS SHORTER (1090 AA) DUE TO A FRAMESHIFT.
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                                                                                                                                     ARLAALEAQLAEKNAELAK
                                                                   TOBAC
                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                          1188
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490
629
                                                                                                                                                                                           Conservative
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                                                                   STANDARD;
                                                                                                                                                                                                                                                          AA;
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Keating C.J., Moran L.S.,
                                                                                                                                                                                                                                                                                                                 468
496
697
                                                                                                                                                                                                      40.48;
57.98;
                                                                                                                                                                                                                                                            136100
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                                                                                                                                                                                                                                                          MW;
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                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                   PPIQIITRNAQEGVYLSKGEQVERISPQ -> ECGKNRSHR
HPGATYCADFRRAGLPLYLFYRGYRRFSDRPGSAYSDHHPQ
                                                                                                                                                                                                                                                                                                   DAVKIALTATPALHTVQIFGEPVYRYTYRTAVIDGFLIDQD
PPIQIITRNAQEGVYLSKGEQVERISPQ -> ECGKNRSHR
                                                                                                                                                                                                                                                                                                                              H-T-H MOTIF (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                            RAGGGLSLQRRAGRAHQ (II
W; CC0423F2A435E578
                                                                   PRT;
                                                                                                                                                                                           Mismatches
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No.
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1.7e+02;
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                                                                                                                                                                                                                    Length 1188;
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(EC 1.3.3.4)

IJ

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RESULT
HMGD_DF
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                       CHAIN
NP_BIND
                      HMGD_DROME STANDARD; PRT; 112 AA. 005783; 09W2D3; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-FEB-1995 (Rel. 31, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HIGH MOBILITY GROUP PROTEIN D (HMG-D). HMGD OR CG17950. HMGD OR CG17950. Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Endopterygota; Diptera; Brachycera; Musco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. SR1;
MEDLINE=97385200; PubMed=9238074;
Lermontova I., Kruse E., Mock H.-P., Grimm B.;
"Cloning and characterization of a plastidal a
                                                                                                                                                                                                                                                                                                                                                                                                   TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyrin biosynthesis; Heme biosynthesis; Oxidoreductase; Transit peptide; Flavoprotein; FAD; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y13465; CAA73865.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta;
Asteridae; euasterids I; Solar
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 Chlorophyll biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoform of tobacco protoporphyrinogen IX oxidase Proc. Natl. Acad. Sci. U.S.A. 94:8895-8900(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROTOPORPHYRINOGEN
                                                                                                                                                                                                                              303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: PENULTIMATE STEP CHLOROPHYLL SYNTHESIS. SUBUNIT: HOMODIMER; CONTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDUCTION: OSCILLATING EXPRESSION DURING DIURNAL GROWTH. MAXI EXPRESSION IN THE DARK PERIOD.
SIMILARITY: BELONGS TO THE PROTOPORPHYRINGGEN OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR: FAD (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: PROTOPORPHYRINOGEN-IX +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION:
DEVELOPMENTAL STAGE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION IX TO FORM PROTOPORPHYRIN IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DECREASED EXPRESSION
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                                                                                                                                                                                                                                                                                                Similarity
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78
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83
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57.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solanales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptophyta; Embryophyta; Traclyta; eudicotyledons; core eudicot
Solanales; Solanaceae; Nicotiana
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                                                                                                                                                                                                                                                                                    Ψ
                                                                                                                                                                                                                                                                                                Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                              Score 41.5;
                                                                                                                                                                                                                                                                                                                                                                      PROTOPORPHYRINOGEN FAD (POTENTIAL).
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                                                                                                                                                                                                                                                                                                              DB
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                          Brachycera; Muscomorpha;
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yelse B.M., Woolage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yelse B.M., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Cibbe B. M., Strong G., Zhao Q., Zheng L.,
RA Yeng X., Zhou X., Zhu X., Smith H.O., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B., Bhandari D., Bolshakov S., Bernan B. P., Bhandari D., Bolshakov S., Bernan B., Bandale J., Brottier D., Bolshakov S., Benos P.V., Berman B., Bhandari D., Bolshakov S., Bernan B., Bandale J., Bayraktarin D., Bolshakov S., Bolshakov S., Bandale J., Bayraktarin D., Bolshakov S., Bolshakov B., Bandale J., Bayraktarin D., Bolshakov S., Bolshakov S., Bandale J., Bayraktarin D., Bolshakov S., Bandale J., Bayraktarin D., Bolshakov S., Bolshakov S., Bandale J., Bayraktarin D., Bolshakov S., Bayraktarin B., Bayrakta Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000). Ner S.S., Churchill M.E.A., Searles M.A., "dHMG-Z, a second HMG-1-related protein i. Nucleic Acids Res. 21:4369-4371(1993). SEQUENCE FROM N.A. STRAIN=CANTON-S; MEDLINE=94021387; Wagner C.R., Hamana K., Elgin S.C.I
"A high-mobility-group protein and
melanogaster."; "HMG-D is an architecture-specific to DNA containing the dinucleotide EMBO J. 14:1264-1275(1995). MEDLINE=95237208; PubMecChurchill M.E.A., Jones associated MEDLINE=94222028; Ner S.S., Travers CHARACTERIZATION. STRAIN=BERKELEY; MEDLINE=20196006; PubMed=10731132; SEQUENCE MEDLINE=92236564; [1] SEQUENCE FROM N.A., Travers A.A.; CHARACTERIZATION. TISSUE-Embryo, EMBO 13:1817-1822(1994) Travers A.A.; he Drosophila melanogaster homologue of the Drosophila melanogaster homologue of the Drosophila melanogaster homologue of 12:1915-1923(1992) PubMed=8414994; PubMed=7720717;
Jones D.N.M., Glaser PubMed=1373803; PubMed=8168480; AND SEQUENCE OF . R.; : protein its 45-77 Τ., cDNAs from Drosophila in Drosophila m that preferentially binds Hefner HMG 1 protein, is absence of histone melanogaster."; Searles z

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RESULT 15
Y458_METJA
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Best Local Similarity
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STRUCTURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR OF 2-74.
MEDLINE-9506330; PubMed-7922039;
MEDLINE-9506330; PubMed-7922039;
Jones D.N.M., Searles M.A., Shaw G.L., Churchill M.E.A.,
Jones D.N., Travers A.A., Neuhaus D.;
"The Solution structure and dynamics of the DNA-binding d
HMG-D from Drosophila melanogaster.";
Structure 2:609-627(1994).
         STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I- FUNCTION: BINDS PREFÉRENTIALLY SINGLE-STRANDED DNA AND UNWINDS
DOUBLE STRANDED DNA, PREFERS SITES CONTAINING THE SEQUENCE 5'-TTG-
3'. FRACILITATES DNA BENDING, ASSOCIATED WITH EARLY EMBRYONIC
CHROMATIN IN THE ABSENCE OF HISTONE H1.
-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- DEVELOPMENTAL STAGES PRESENT IN ALL STAGES OF DEVELOPMENT.
-I- SIMILARITY: BELONGS TO THE HMG1/HMG2 PROTEIN FAMILY.
-I- SIMILARITY: CONTAINS 1 HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SEQUENCE
                                                                                                                                                                                                                                       MJ0458
                                                                                                                                                                                                                                                                     01-NOV-1997
20-AUG-2001
                                                                                                                                                                                                                                                                                                   Q57900;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00505; HMG_box; 1. SMART; SM00398; HMG; 1.
                                                                                                                                                                       NCBI_TaxID=2190;
                                                                                                                                                                                       Methanococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0004362; HmgD.
InterPro; IPR000910; HMG_12_box.
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                         Archaea;
                                                                                                                                                                                                                        Methanococcus
                                                                                                                                                                                                                                                        HYPOTHET ICAL
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A44382; A44382.
S32724; S32724:
IHMA; 31-JUL-94.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SIARLGG--KLAKLAKKLAKLAK 23
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                                                                                                                                                                                                        Euryarchaeota;
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112 AA;
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
PROTEIN MJ0458.
                                                                                                                                                                                                                        jannaschii
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosomal protein; DNA-binding; 3D-structure. 71 HMG BOX.
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12416 MW;
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; 3F537CCFD62FEC9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                    216 AA
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Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001048; Aakinase. Pfam; PF00696; aakinase; 1. Hypothetical protein; Complete SEQUENCE 216 AA; 24080 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67496; AAB98446.1; ...
TIGR; MJ0458; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus
Н
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MHIVKIGGSLTYDAKPLLKALK
                                              MSIARLGGKLAKLAKKLAKLAK
                                                                                                                                                                    l Similarity 45.9
10; Conservative
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45.5%;
22
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37856E333F3D2A76 CRC64;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Perfect score:
Sequence:
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1: sp_archea:*
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4: sp_human:*
5: sp_invertebrate
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7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
1: Sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	47	45.2	459	σ.	Q04011	Q04011 wuchereria
2	47	45.2	981	2	Q9PR04	Q9pr04 ureaplasma
ω	45	43.3	364	N	Q9KID1	
4	45	43.3	475	N	Q53164	_
υı	45	43.3	1177		Q9V1R8	_
0	45	43.3	1262	տ	Q9N3T9	Q9n3t9 caenorhabdi
7	44	42.3	68	12	Q9QJE6	\mathbf{a}
80	44	42.3	360	ν	P70906	P70906 borrelia he
9	44	42.3	454	N	Q9Z902	Q9z902 chlamydia p
10	44	42.3	454	N	Q9JRZ3	Q9jrz3 chlamydia p
11	43.5	41.8	548	N	Q9JYK0	_
12	43	41.3	104	Ν	084119	084119 chlamydia t
13	43	41.3	114	N	Q9JY43	
14	43	41.3	246	G	Q93548	Q93548 caenorhabdi
15	43	41.3	307	N	Q9HT75	
16	43	41.3	412	N	Q9ZMV5	
17	43	41.3	824	ພ	Q9KY12	Q9ky12 streptomyce
18	43	41.3	999	9	021882	021882 bacteriopha
19	43	41.3	1027	N	Q9AAQ1	Q9aaq1 caulobacter

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ALIGNMENTS

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SEQUENCE
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"Surface protein variation by expression site
relapsing fever agent Borrelia hermsii.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ
EMBL; AF230049; AAF73349.1;
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EMBL; AE002114; AAF30546.1; ..
InterPro; IPR003349; ABC_transportr.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
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MEDLINE=20500219; Pub:
Glass J.I., Lefkowitz
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Plasmid 1p28.
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witz E.J., Glass
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UPTAKE HYDROGENASE.
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"Isolation of regulatory mutants in photosynthesis gene expression Rhodobacter sphaeroides 2.4.1 and partial complementation of a Prremutant by the HupT histidine-kinase.";
Microbiology 141:1805-1819(1995).
EMBL; Y14197; CAA74585.1;
EMBL; Y14197; CAA74585.1;
EMBL; P21852; AAA99491.1;
EMBL; P21852; H2A.
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Rhodobacter sp
                                                                                                "pyrococcus abyssi genome sequence: insights i structure and evvolution."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ EMBL; AJZ48284; CAB49281.1; -. InterPro; IPR003405; ABC_transportr. InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
                                                                                                                                                                                                                     Pyrococcus abyssi.
Archaea; Euryarchaeota;
NCBI_TaxID=29292;
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STRAIN=2.4.1;
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Submitted (
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[2]
                                                                                                                                                                                                                                                                                             Q9QJE6
Q9QJE6;
Q1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL/GenBank
EMBL; AC024791; AAF60651.1; -.
InterPro; IPR001064; CryStallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA;
SEQUENCE 1262 AA; 144120 MW; 4CBAABS
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01-OCT-2000 (TremBLrel.
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Y47G6A.12 PROTEIN.
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"Genetic analysis of HIV-1 Spanish isolates.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ
EMBL; AF152816; AAF08454.1; -.
InterPro; IPR000777; GP120.
                                                                                                                                                                                 Human immunodeficiency virus Viruses; Retroid viruses; Ret NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted [3]
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"The sequence of C. (
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                   STRAIN-I20N;
                                                                                                                                                                                                                                                          ENV
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               ENVELOPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
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                                                                                         opez-Galindez C.;
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elegans cosmid Y47G6A.";
) to the EMBL/GenBank/DDBJ
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Last annotation updat
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4CBAAB9E0330CEB3 CRC64;
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P70906;
01-FEB-1997 (TrEMBLrel. 0:
01-FEB-1997 (TrEMBLrel. 0:
1 01-JUN-2001 (TrEMBLrel. 1:
01-JUN-2001 (TREMBLREL. 1:
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Best Local :
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Best Local
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Olinger L., Grimwood J., Davis R.W., Ste
"Comparative genomes of Chlamydia pneumo
Nat. Genet. 21:385-389(1999).
EMBL; AE001604; AAD18335.1; -.
HSSP; P24182; IBNC.
InterPro; IPR000901; CPSase.
Pfam; PF00289; CPSASE_L_Chain; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
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Restrepo B.I., Carter C.J., Infante D
Submitted (MAR-1996) to the EMBL/GenB
EMBL; U52149; AAB17739.1;
InterPro; IPRO00680; Borrelia_lipo.
Pfam; PF00921; Lipoprotein_2; 1.
SEQUENCE 360 AA; 36906 MW; 86204D
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01-MAY-1999 (Tremblr
01-JUN-2001 (Tremblr
BIOTIN CARBOXYLASE.
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                                                                                                                                          MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Olinger L., Grimwood J., Davis R.W.,
                                                                                                                                                                                                                                                                                    Chlamydia pneumoniae (Cl
Bacteria; Chlamydiales;
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Bacteria; Spirochaetales;
                                                                                                                                                                                                        STRAIN=CWL029;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=83558;
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8 AA;
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Last annotation updat
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Pred. No. 1.8e+02;
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86204DE08F4EEA38
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                                                                                                                                                Fan J., Hyman R.W.,
R.S.;
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Q9JYK0;
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PROSITE; PS00867; CPSASE_2; UNKNC
SEQUENCE 454 AA; 50092 MW; 9D
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Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AP002545; BAA983392.1; -.
EMBL; AE002217; AAF38404.1; -.
TIGR; CP0586; -.
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Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishi K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
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EMBL; AE002505; AAF41903.1; -.
TIGR; NMB1548; -
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STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel
Stephens R.S., Kalman S., Tatuso
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01-NOV-1998 (TrEMBLIEL 08, La
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MEDLINE-20175755;
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EMBL; AE001285; AAC67708.1; -.
Hypothetical protein; Complete
SEQUENCE 104 AA; 10436 MW;
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                                                                                                                                                                                                                                                         Length 104;
                                                                                                                                                                                                                                                                                                                         CRC64;
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Best Local
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093548:
01-FEB-1997 (TrEMBLrel. C
01-FEB-1997 (TrEMBLrel. C
01-JUN-2001 (TrEMBLrel. 1
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SEROGROUP B;

STRAIN-MC58 / SEROGROUP B;

MEDLINE-2017575; PubMed-10710307;

MEDLINE-2017575; PubMed-10710307;

MEDLINE-2017575; PubMed-10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougharty B.A.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougharty B.A.,

MASON T., Ciecko A., Parkeey D.S., Blair E., Cittone H., Clark E.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
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01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                          Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Ratson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                 elegans.";
Nature 368:32-38(1994)
                                            Watson A., Weinstock L., Wilkinson 2.2 Mb of contiguous nucleotide
                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:1809-1815(2000).
EMBL; AE002525; AAF42096.1;
TIGR; NMB1755; -.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=94150718; pubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                 F21G4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete SEQUENCE 114 AA; 13184 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta suk
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 Z81016; CAB02663.1;
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(TIEMBLrel. 15, Last sequence update)
(TIEMBLrel. 15, Last annotation update)
L PROTEIN NMB1755.
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                                                                                                                                                                                                                                                                                                                                                                             Peloderinae;
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4; Mismatches
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subdivision; Neisseriaceae; Neisseria.
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75C791CD480842D4
                                                   sequence
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01-MAR-2001
01-MAR-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                            Complete SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004962; AAG08883.1; -
InterPro; IPR001987; Lipoprotein_4.
Pfam; PF01297; Lipoprotein_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opportunistic pathogen.";
Nature 406:959-964(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=287;
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149 GKIAKVDKKTAKTVK 163
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307 AA;
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                                                                                                                                                                                                                       Score 43; Db 2, Pred. No. 2.1e+02;
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Pred. No. 1.7e+02;
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Page 6

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 8, 2002, 13:33:37; Search time 12.86 Seconds (without alignments) 136.238 Million cell updates/sec Run on:

CHIMERA 104 1 SMSIARLGGKLAKLAKKLAKLAK 23 Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	Ω	Description
-	47	45.2	981	5	C82930	pl15 protein UU140
7	45	43.3	362	7	I40304	outer membrane lip
9	45	43.3	462	~	T17948	ABC transporter pr
4	45	43.3	1177	7	B75150	a
S	44	42.3	454	~	E72110	biotin carboxylase
9	44	42.3	454	~	F86513	biotin carboxylase
7	44	42.3	454	7	G81560	acetyl-coenzyme A
80	43.5	41.8	548	7	A81070	tspB_protein, prob
6	43	41.3	104	7	H71555	hypothetical prote
10	43	41.3	114	~	B81046	
11	43	41.3	246	7	T21215	
12	43	41.3	307	N	C82959	
13	43	41.3	337	~	C10990	hypothetical prote
14	43	41.3	412	~	D71972	hypothetical prote
15	43	41.3	755	7	S32103	filensin - bovine
16	43	41.3	790	7	JC5749	DNA topoisomerase
17	43	41.3	1722	-	178879	retinoblastoma bin
18	42	40.4	247	~	A75254	conserved hypothet
19	42	40.4	273	Н	R5ZM2	ribosomal protein
20	42	40.4	293	1	DDBP32	helix-destabilizin
21	42	40.4	293	1	DDBP36	helix-destabilizin
22	42	40.4	352	7	S16547	neutral proteinase
23	42	40.4	457	7	H71553	probable biotin ca
24	42	40.4	457	7	D81708	acetyl-coenzyme A
25	42	40.4	785	7	S63652	hypothetical prote
56	42	40.4	953	~	S75285	
27	42	40.4	1188	Н	NDECKR	type I site-specif
28	42	40.4	1616	7	T47801	
29	42	40.4	3534	7	T42567	tegument protein 2

protoporphyrinogen high mobility grou	hypothetical prote hypothetical prote	conserved hypothet	outer membrane cla	hypothetical prote	outer membrane pro	outer membrane pro	probable heat shoc	cmk protein precur	hypothetical prote	hypothetical prote	DNA repair protein	variable major pro
T04058 A44382	A75187 B64357	F69526	A37004	T27867	A81782	C81205	F85616	D64830	B86133	G96590	T43507	S11981
77	7	010	0	7	7	N	~	N	7	7	7	7
548 112	140 216	221	240	241	242	242	262	262	293	353	354	364
39.9 39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4
41.5	4 1 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	41	41	41	41	41	41	41	41	41	41	41
30 31	3 8 3 8 7	3.34	36	37	38	39	40	41	42	43	44	45

Н

RESULT

C82930	
p115 protein UU140 [imported] - Ureaplasma urealyticum	
C;Species: Ureaplasma urealyticum	
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000	
C; Accession: C82930	
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.	
submitted to GenBank, February 2000	
A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a	ฮ
A; Reference number: A82870	
A; Accession: C82930	
A;Status: preliminary	
A; Molecule type: DNA	
A; Residues: 1-981 <gla></gla>	
A; Cross-references: GB: AE002114; GB: AF222894; NID: q6899086; PIDN: AAF30546.1; GSPDB: GN	GN
A; Experimental source: serovar 3; biovar 1	
C;Genetics:	
A;Gene: p115; UU140	
A; Genetic code: SGC3	
Query Match 45.2%; Score 47; DB 2; Length 981;	
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;	
Qy 3 SIARLGGKLAKLAKLAK 23	
DD 188 NLARLNDIVANLKKELAKLQK 208	

RESULT 140304

it would be a controlled by the control of the cont ö Gaps ; Score 45; DB 2; Length 362; Pred. No. 55; 4; Mismatches 8; Indels Query Match 43.3%; Best Local Similarity 45.5%; Matches 10; Conservative

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recosts

biotin carboxylase [imported] - Chlamydophila pneumoniae (strain J138)

C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C; Accession: F86513

R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;

Nucleic Acids Res. 28, 2311-2314, 2000

A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A; Accession: F86513

A; Cross-references: GB: BA000008; NID: g8978555; PIDN: BAA98392.1; GSPDB: GN00142

A; Experimental source: strain J138

C; Genetics:

A; Gene: accC

C; Superfamily: biotin carboxylase; biotin carboxylase homology
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe, M. Tille: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <REA>
A;Reference number: A72000; MUID:99206606
A;Accession: E72110
A;Status: preliminary
A;Nolecule type: DAN
A;Residues: 1-454 AARN
A;Residues: 1-454 AARN
A;Cross_references: GB:AE001604; GB:AE001363; NID:g4376438; PIDN:AAD18335.1; PID:g437
A;Cross_references: Strain CWL029
C;Genetics:
A;Gene: acc
A;Gene: acc
C;Superfamily: biotin carboxylase; biotin carboxylase homology
F;3-448/Domain: biotin carboxylase homology <BCH>
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A,Experimental source: strain AR39, HL cells
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A;Gene: CP0586
C;Superfamily: biotin carboxylase; biotin carboxylase homology
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93;
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Pred. No. 9
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56.5%;
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Best Local Similarity
Matches 13; Conserv
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R;anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: B75150
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A,Molecule type: DNA
A,Residues: 1-1177 <KAW>
A,Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49281.1; PID:9545779
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E72110
biotin carboxylase - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Bate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: E72110
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
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                                                                                                                                                                                                                                     ABC transporter protein homolog A445L - Chlorella virus PBCV-1 C; Species: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999 C; Accession: T17948 R; Graves, M.V.; Van Etten, J.L. submitted to the BMBL Data Library, May 1999 A; Reference number: 218806 A; Reference number: 218806 A; Reference number: preliminary; translated from GB/EMBL/DDBJ A; Release: DNA A; Residues: 1-462 <GRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96813.1 A;Experimental source: specific host Chlorella strain NC64 C;Genetics: A;Note: A445L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 462
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C;Superfamily: chromosome segregation protein SMC1
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Pred. No. 68;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 MGVIKSGGSVARLKKAIPKIKK 330
                                                                             :: || || :|||| 268 ALKFARGGGNAGQLAKEAAKAA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MSIARLGGKLAKLAKKLAK 23
                                                  1 SMSIARLGGKLAKLAKKLAKLA 22
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Best Local Similarity 50.0
Matches 10; Conservative
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Best Local Similarity
"has 8; Conserve
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C;Accession: B81046
R;Tettelin, H; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R;Tettelin, H; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoll, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20178755
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <TET>
A;Residues: 1-114 <TET>
A;Cross-references: GB:AE002525; GB:AE002098; NID:g7227004; PIDN:AAF42096.1; PID:g722
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable adhesin PA5498 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Dacies: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C82959
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. inture 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
       hypothetical protein NMB1755 [imported] - Neisseria meningitidis (strain MC58 serogro
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A;Cross-references: EMBL:281016; PIDN:CAB02663.1; GSPDB:GN00028; CESP:F21G4.4
A;Experimental source: clone F21G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T21215
                                        C.Species: Neisseria meningitidis
C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.3%; Score 43; DB 2;
llarity 47.6%; Pred. No. 36;
Conservative 4; Mismatches
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2; Mismatches
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A; Introns: 31/3; 113/3; 175/3; 197/3
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55 AIADLAGEMRRLAKKSKMLLK 75
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                           C; Accession: H71555
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac A; Reference number: A71570; MUID:99000809
A; Reference number: A71570; MUID:99000809
A; Accession: H71555
A; Accession: H71555
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-104 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE002505; GB:AE002098; NID:g7226794; PIDN:AAF41903.1; PID:g7226796; Experimental source: serogroup B, strain MC58 C;Genetics: A;Genetics: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE001285; GB:AE01273; NID:g3328507; PIDN:AAC67708.1; PID:g332851
A;Experimental source: serotype D, strain UW-3/Cx
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C; Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 28-Jul-2000
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Gene: CT117
C;Superfamily: Chlamydia trachomatis hypothetical protein CT117
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       Length 454;
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Pred. No. 1.3e+02;
4; Mismatches 6;
Score 44; DB 2;
Pred. No. 93;
2; Mismatches
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                                                                                                                                                                                     106 SESIAMMGDKIA--AKSLAKKIK 126
                                                                                                                                             1 SMSIARLGGKLAKLAKKLAKLAK 23
   42.3%;
56.5%;
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41.8%;
Best Local Similarity 44.4%;
Matches 12; Conservative
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SLGRVVGALAKVAKLVVALA 44
                                                                        13; Conservative
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Matches 10; Conserv
                                        Best Local Similarity
       Query Match
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Gaps

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6; Mismatches

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A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0110
C;Superfamily: Helicobacter pylori hypothetical protein HP0120
                                                                                                                                                                                                                                                        41.3%; Score 43; DB 2; Length 412; 38.1%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 GGKISKAFEKLGKMIK 446
                                                                                                                                                                                                                                                                                                                                               8; Conservative
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Matches 8; Conserv
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Job time: 124 sec
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A;Experimental source: strain PAO1
C;Genetics
A;Gene: PAO498
C;Superfamily: hypothetical protein H10119
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R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor., R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor., R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature, Squares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Althors: Squares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Reference number: A70500; MUID: 98295987
A; Accession: C70990
A; Status: preliminary: nucleic acid sequence not shown; translation not shown A; Molecule type: DAA
A; Residues: 1-337 <COL.>
A; Assidues: 1-337 <COL.>
A; Assidues: 1-337 <COL.>
A; Accession: C70990
A; Status: preliminary: nucleic acid sequence not shown; translation not shown A; Molecule type: DAA
A; Cross-references: GB:295150; GB:AL123456; NID: 93250708
A; Experimental source: strain H37Rv
A; Rote: this ORF is annotated but not translated in GenBank entry MTCY164, release 106
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A;Molecule type: DNA
A;Molecules: 1-412 ASRN>
A;Cross-references: GB:AE001450; GB:AE001439; NID:g4154617; PIDN:AAD05689.1; PID:g415461
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A;Reference number: A71800; MUID:99120557
A;Accession: D71972
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Jun-2000
C;Accession: D71972
C;Accession: D71972
S;Alm, K.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
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C;Species: Mycobacterium tuberculosis
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
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97;
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90;
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Pred. No.
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Pred. No.
A; Reference number: A82950; MUID:20437337
A; Accession: C82959
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Best Local Similarity 43.5%;
Matches 10; Conservative
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Best Local Similarity 58.00,
The State of the
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180 RLGGLDGKLRERLGKLA 196
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A;Start codon: GTG
F;194/Region: amber stop codon
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                                                                                                                                                                          A; Residues: 1-307 <STO>
                                                                                       A;Status: preliminary
                                                                                                                          A; Molecule type: DNA
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Niterant anaes: intermediate filament protein
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Date: (Oc-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997
C; Accession: S32103; A40690
R; Gounari, F.; Merdes, A.; Quinlan, R.; Hess, J.; FitzGerald, P.G.; Ouzounis, C.; Geo submitted to the EMBL Data Library, March 1993
A; Description: Bovine filensin possesses primary and secondary structure similarity the A; Reference number: S32103
A; Accession: S32103
A; Reference number: S32103
A; Residues: 1-755 <GOUD
A; Reference number: A40690; MUD:9287751; PID:9287752
B; Gounari, F.; Mardes, A.; Quinlan, R.; Hess, J.; FitzGerald, P.G.; Ouzounis, C.A.; G
J; Cell Biol. 121, 847-853, 1993 ·
A; Title: Bovine filensin possesses primary and secondary structure similarity to inte A; Reference number: A40690; MUD:93260017
A; Accession: A40690
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-622, RPP, 625-755 <GO2>
A; Experimental source: lens
A; Residues: 1-622, RPP, 625-755 <GO2>
A; Resperimental source: lens
A; Residues: 1-622, RPP, 625-755 <GO2>
A; Newerlas: membrane-associated from NCBI backbone (NCBIN:132495, NCBIP:132499)
A; Note: part of this sequence was confirmed by protein sequencing
C; Keywords: membrane-associated protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 2;
Pred. No. 2e+02;
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50.0%;
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Sequence

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US-07-908-455A-15 US-08-445-120-41 US-07-908-455A-21 US-07-908-455A-23 US-07-908-455A-62 US-08-434-120-53 US-08-434-120-53 US-08-434-120-53 US-08-445-325-53 US-08-465-325-53 US-08-465-325-86 US-08-944-133-21 US-08-944-133-21 US-08-944-133-21 US-08-944-133-21 US-08-944-133-21 US-08-94-133-08 US-08-95-171-40 US-08-689-486-45

ALIGNMENTS

27, 62, 53, 53, 53, 40,

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; Search time 12.46 Seconds
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                Compugen Ltd.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
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104
1 SMSIARLGGKLAKLAKKLAK
                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                        Title:
Perfect score:
Sequence:
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DB sed
                                                                                                                                                                                                  Scoring table:
                                                         protein -
                                                                                                                                                                                                                                                                    Total number
                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                Minimum
                                                                                                                                                                                                                                                                                                                Maximum
                                                                                   Run on:
                                                       ΜO
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/cgn2_6/ptodata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/pcTUS_COMB.pep:*

Issued_Patents_AA:*

Database

Description sednence sed Sequence US-08-944-133-7
US-08-944-133-8
US-08-944-133-8
US-08-944-133-8
US-08-944-133-27
US-08-944-133-6
US-08-944-133-6
US-08-944-133-6
US-08-944-133-6
US-08-944-133-6
US-08-944-133-8
US-08-944-133-39
US-08-944-133-25
US-08-944-133-25
US-08-944-133-25
US-08-944-133-39
US-08-944-133-39
US-08-944-133-39
US-08-944-133-39
US-08-944-133-25 DB Length Query Match Score Š

28,

258, 28, 28, 28, 28, 28,

88

CITY: Baron Rouge STATE: LA COUNTRY: USA ZIP: 70821-2471 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25	CONTENT OF TELLING DATE: US/08/944,133	REGISTRATION NUMBER: 33451 REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301 TELECOMMUNICATION INFORMATION: TELEPHONE: 504 387-3221 TELEPHONE: 504 346-8049 INPORMATION FOR END ID No. 7: SEQUENCE CHARACTERISTICS: LENGTH: 21 amino acids TYPE: amino acid STANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
nted,	Appli Appli Appli 7, Appli 6, Appl Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli	Appl Appl Appli Appl Appl Appl Appl Appl

Length 21;

DB 1;

Score 72;

69.28;

Query Match

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REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOURNER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE: US/08/681,075
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
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80.0%; Pred. No. 0.00033;
tive 2; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/08944133
Patent No. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: Amphipathic Peptides NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
2IP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. BOX 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 IARLGGKLAKLAKKLAKLAK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LAKLAKKLAKLAKLAK 21
                                                                                                                                                    ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Runnels, John H
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                               Baton Rouge
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Matches 16; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                      USA
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                                                                                               CITY: Batc
STATE: LA
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                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-944-133-8
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                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-007-1997
FLING DATE: 06-007-1997
FLING DATE: 07-007-1997
FLING DATE: 08-007-1997
FLING APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE: 22-APR-1994
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72; DB 1; Ler
Pred. No. 0.00033;
  Best Local Similarity 80.0%; Pred. No. 0.00025; Matches 16; Conservative 2; Mismatches 2;
                                                                                                                                                                                         Sequence 4, Application US/08944133
Patent No. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-944-133-8
Sequence 8, Application US/08944133
Patent No. 5789542
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                STREET: Dohn H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: At
TELECOMMUNICATION INFORMATION
TELEPHONE: 504 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                           4 IARLGGKLAKLAKKLAKLAK 23
                                                                               2 LAKLAKKLAKLAKKLAKLAK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 IARLGGKLAKLAKKLAKLAK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 28 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserva
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                                                                                                                                                         RESULT 2
US-08-944-133-4
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Length 28;

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Pred. No. 0.0013;
2; Mismatches 2; Indels
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Pred. No. 0.0017;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: LA
COUNTRY: USA
ZIP: 70821-2471
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 346-8049
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
WUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-OCT-1997
CLASSIPRICATION: 5330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08944133 Patent No. 5789542
                                                                                                                                                                                                                                                        64.48;
78.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                       4 IARLGGKLAKLAKKA 22
                                                                                                                                                                                                                                                                                                                                                                            3 LAKLAKKLAKLAKKA 21
                 TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.57
Best Local Similarity 83.37
Matches 15; Conservative
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-944-133-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-944-133-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                  TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
JS-08-944-133-3
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                                                                                                                                     FILING DATE:
APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: RUNDELS, John H
REGISTRATION NUMBER: 33451
FREFERENCE/DOCKET NUMBER: 3451
FREEDRUNG-TOOK INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHONE: 504 387-3221
FREEDRAX: 504 346-8049
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72; DB 1; Length 28;
Pred. No. 0.00033;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
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COMPARIS.

ID: 70821-2471

COMPUTER READBLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,133

FILING DATE: 06-0CT-1997

CLASSIFICATION: 5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/08944133
Fatent No. 5789542
GENERAL INFORMATION:
APPLICANT: MCLAUGHIIN, MARK L
APPLICANT: BECKER, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. BOX 2471
STREET: LA
                                CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/944,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.2%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: peptide
US-08-944-133-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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Patent No. 5635479
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baker, Margaret A.
APPLICANT: Maloy, W. Lee
TITLE OF INVENTION: Treatment of Gynecological
TITLE OF INVENTION: Malignancies with
TITLE OF INVENTION: Biologically Active Peptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Carella, Stewart
ADDRESSEE: Cacchi & Stewart
ADDRESSEE: Cacchi & Stewart
TITLE OF INVENTION: USES Therefor NUMBER OF SEQUENCES: 89
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADBRESSEE: Carella, Byrne, Bain, Gilfillan, STREET: New Jersey
COUNTRY: USA
ZIP: 07068
COMBUTER: New Jersey
COMBUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2
COMBUTER: IBM PS/2
OPERATING SYSTEM: US/07/908,455A
FILING DATE: 19920702
CLASSIFCATION NUMBER: US 0746629
FILING DATE: 13-APR-1991
APPLICATION NUMBER: US 07476629
FILING DATE: 18-APR-1991
APPLICATION NUMBER: 24,025
FILING DATE: 108-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Eillot M
REGISTRATION NUMBER: 24,025
TELECOMMUNICATION INFORMATION:
TELEFAN: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: AMINO ACID
STRANDENESS:
TOPPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62; DB 1;
Pred. No. 0.0064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: amide-terminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.6%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07068
COMPUTER READABLE FORM:
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APPLICANT: Berkowitz, Barry A.
APPLICANT: Rari, U. Prasad
APPLICANT: Maloy, W. Lee
TITLE OF INVENTION: No. 5459237el Peptide Compositions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.6%; Score 62; DB 1; Length 14; 100.0%; Pred. No. 0.0044; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John HON:
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/681,075
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                                               Sequence 6, Application US/08944133
Patent No. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-07-908-455A-4
; Sequence 4, Application US/07908455A
; Patent No. 5459237...
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                           Query Match 59.6
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-944-133-6
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Patent No. 5856178
GENERAL INFORMATION:
APPLICANT: White Phb, Kenneth
APPLICANT: Reed, William
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask Britt and Rossa
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                                                                                                                                                                                                                                                                                                                                                       Length 21;
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                                                                                                                                                                                                                                                                                                                                     Score 62; DB 1; Len
Pred. No. 0.0064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
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                                                                                              REFERENCE/DOCKET NUMBER: 05387.0021-03000 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4400 INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY.
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FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SWELGETT PDD, SUSAN ERGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
                                                                             32,984
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         59.6%;
82.4%;
                  FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: FORDIS, Jean B
REGISTRATION NUMBER: 32,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not relevant
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Best Local Similarity 82.4'
Matches 14; Conservative
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; MOLECULE TYPE: peptide
US-08-465-325-30
    APPLICATION NUMBER:
                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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US-08-723-306-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Magainin Pharmaceuticals Inc.
APPLICANT: 510 Campus Drive
APPLICANT: 510 Campus Drive
APPLICANT: 510 Campus Drive
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I. Street, N.W. Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
RECISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 421250-194
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
                                                         SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,120
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/297,950
                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: US/08/226,108
FILING DATE:
APPLICATION NUMBER: US/07/937,462
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FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/08465325 Patent No. 5686563 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 RLGGKLAKLAKKLAKLA 22
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Best Local Similarity 82.4
Matches 14; Conservative
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MOLECULE TYPE: peptide
US-08-434-120-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-465-325-30
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ADDRESSEE: Trask Britt and Rossa STREET: P.O. Box 2550
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COUNTRY: USA
                                                       Utah
                                                                                                                                                                                                                                     FILING DATE:
                                                                                      84110
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PCT-US96-10041-28
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                                                   STATE: U COUNTRY:
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                    Gaps
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APPLICANT: White PhD, Kenneth
APPLICANT: White PhD, John
APPLICANT: Morrey PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SQUENCES:
ADDRESSE: Trask Britt and Rossa
STREET: P.O. Box 2550
CTTY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/08723306
Patent No. 5856178
GENERAL INFORMATION:
APPLICANT: White Phb, Woneth
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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Pred. No. 0.007;
                  4; Indels
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APPLICATION NUMBER: PCT/US96/10041
Best Local Similarity 70.0%; Pred. No. 0.007;
                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 8015321922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 8015319168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cch 59.6%; al Similarity 70.0%; 14; Conservative ;
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                                                                                      2 LKKLAKKLKKLAKKLAKLAK 21
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                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             STATE: Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
TELEFAX: 8
                                                                                                                                          RESULT 12
PCT-US96-10041-27
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US-08-723-306-28
                  Matches
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Gaps
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GENERAL INFORMATION:
APPLICANT: White Phb, Kenneth
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SQUENCES: 32
CORRESPONDENCE ADDRESS:
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Pred. No. 0.0097;
1; Mismatches 3; Indels
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                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Trask Britt and Rossa
STREET: P.O. Box 2550
CITY: Salt Lake City
                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweigert Phb, Susan E
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801531922
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| || || || || || || || || || || 4 KLAKKLKKLAKKLAK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.7
Best Local Similarity 77.8
Matches 14; Conservative
STREET: P.O. Box 255
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 8015319168
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Sequence 2, Application US/07908455A

Batch No. 3459237

GENERAL INFORMATION:

APPLICANT: Maloy, W. Lee

APPLICANT: Maloy, W. Lee

TITLE OF INVENTION: No. 5459237el Peptide Compositions and
TITLE OF INVENTION: No. 5459237el Peptide Compositions and
TITLE OF INVENTION: Wo. 5459237el Peptide Compositions and
TITLE OF INVENTION: Wo. 5459237el Peptide Compositions and
TITLE OF INVENTION: USes Therefor
NUMBER OF SEQUENCES:

ADDRESSEE: Cacclla, Byrne, Bain, Gilfillan,
STREET: Beachand
STATE: Reseland
STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER: 134 PS. 5 inch diskette
COMPUTER: 134 PS. 7 inch diskette
COMPUTER: 135 inch diskette
COMPUTER: 135 inch diskette
COMPUTER: 135 inch diskette
COMPUTER: 135 inch diskette
COMPUTER: 136 PS. 50702

STATE: DW4.V2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 07476629

FILING DATE: 135 PR-1991

APPLICATION NUMBER: US 07476629

FILING DATE: 16 PETB-190

ATTORNEY AGENT INFORMATION:

NAME: 015240, E1104

TELEPRAN: ACTORNEY AGENT INFORMATION:

REGISTRANICATION NUMBER: 24,025

REFERENCE OFFER NUMBER: 24,025

RELEPRAN: 201-994-1704

INFORMATION PODE FOR NOW.
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                                                                                                                                                                                                                                                                                                     Score 61, DB 5; Length 23;
Pred. No. 0.0097;
1; Mismatches 3; Indels
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                                              28:
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                                                                                                                                                                                                                                                                                                     Query Match 58.7%;
Best Local Similarity 77.8%;
Matches 14; Conservative
                 | INFORMATION FOR ESQ ID NO: 28
| INFORMATION FOR ESQ ID NO: 28
| SEQUENCE CHARACTERISTICS: |
| ENGTH: 23 amino acids |
| TYPE: amino acid |
| STRANDEDNESS: |
| MOLECULE TYPE: peptide |
| HYPOTHETICAL: YES |
| PCT-US96-10041-28
                                                                                                                                                                                                                                                                                                                                                                                                  6 RLGGKLAKLAKKLAK 23
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US-07-908-455A-2
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Ouery Match 57.7%; Score 60; DB 1; Length 21;
Best Local Similarity 57.9%; Pred. No. 0.012;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 4 IARLGGKLAKKLAKKLA 22

Qy 2 INKIAGKLAKIAKKLA 20

Db 2 IAKIAGKIAKIAKIA 20
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Search completed: May 8, 2002, 13:34:22 Job time: 550 sec

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May 8, 2002, 07:20:14 ; Search time 35.89 Seconds (without alignments) 28.529 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             473505 seqs, 146272329 residues
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                          US-09-765-086-207
30
1 SMSIARL 7
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Maximum DB seq length: 2000000000
                                                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                 Run on:
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SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_nammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P77850 chlamydia t	084705 chlamydia t	Q9plm7 chlamydia m	Q9c6f0 arabidopsis	065663 arabidopsis	Q9yct2 aeropyrum p	068069 rhodobacter	Q9cse0 mus musculu	Q90417 brachydanio	Q9bu29 homo sapien	Q12205 saccharomyc	Q9h0h0 homo sapien	Q9uld3 homo sapien	Q9syi4 arabidopsis	Q85057 peanut stri	Q85071 peanut stri	Q9u175 leishmania	097096 clonorchis	Q9zwb5 arabidopsis
SUMMARIES	OI	P77850	084705	Q9PLM7	Q9C6F0	065663	Q9YCT2	690890	Q9CSE0	990417	Q9BU29	012205	0н0н6Ф	Q9ULD3	Q9SY14	085057	985071	Q9U175	960260	Q9ZWB5
	DB	7	7	7	10	10	-	7	11	13	4	æ	4	4	10	12	12	S	S	10
	Query Match Length DB	301	301	301	329	369	305	307	317	422	571	849	1204	1209	1216	3222	3222	3475	212	213
ð	Query Match	90.06	90.0	90.0	90.0	90.0	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	83.3	83.3
	Score	27	27	27	27	27	56	26	26	26	26	56	26	26	26	36	26	26	25	25
	Result No.	п	7	m	4	Ŋ	9	7	8	σ	10	11	12	13	14	15	16	17	18	19

20 25 83.3 255 3 013888 21 25 83.3 259 5 992175 22 25 83.3 259 5 991933 23 25 83.3 259 5 991934 24 25 83.3 259 5 991935 25 25 83.3 259 2 091128 26 25 83.3 294 2 055529 27 25 83.3 599 10 094287 28 25 83.3 668 12 096427 29 25 83.3 668 12 096402 31 24 80.0 107 2 091195 32 24 80.0 210 12 06448 33 24 80.0 210 12 064748 34 24 80.0 239 2 036763 35 24 80.0 239 2 036763 36 24 80.0 239 2 036763 37 24 80.0 239 2 036763 38 24 80.0 239 2 036763 39 24 80.0 239 2 036763 41 24 80.0 331 2 094644 43 24 80.0 331 2 094644 44 24 80.0 331 2 094644 45 24 80.0 331 2 094644
255 883 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
010m4v0/000010m4v0/000010m4v

ALIGNMENTS

			Gaps		
			ő		
0 277850 PRELIMINARY; PRT; 301 AA. 277850:	01.FEB-1997 (TrEMBLrel. 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) PHOSPHATIDYLSERINE DECARBOXYLASE (EC 4.1.1.65).	Chlamydia trachomatis. Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia. Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia. NCBLTaxID=813; NCBLTaxID=813; SEQUENCE FROM N.A. SEGUENCE FROM N.A. SEQUENCE (SEP-1996); to the EMBL/GenBank/DDBJ databases. -!- CATALYTIC ACTIVITY: PHOSPHATIDYL-L-SERINE - PHOSPHATIDYLETHANOLAMINE + CO(2). -!- COFACTOR: PYRIDOXAL, PHOSPHATE OR PYRUVATE.	### PF02666; PS_DCarbxylase. Lyase. Lyase. SEQUENCE 301 AA; 34064 MW; A4E852492F408207 CRC64; Query Match Best Local Similarity 85.7%; Pred. No. 56; Marches 6; Conservative 1; Mismatches 0; Indels	1 SMSIARL 7 : 158 SMAIARL 164	T 2 5084705 PRELIMINARY; PRT; 301 AA. 084705; Created) 01.NOV-1998 (TrEMBLEL. 08, Created) 01.NOV-1998 (TrEMBLEL. 08, Last sequence undate)
P77850 ID P	E	CCCCF ACCOCC	DR DR SQ Que Bes Mat	Oy Dp	RESULT 084705 ID O AC O DT 0

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Dioxygenase.
SEQUENCE 3
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Q9C6F0;
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STARIN-MODN / NIGG;
MEDLINE-20150255; Pubbed-10684935;
REad T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
pneumoniae.AR39.";
                                                                                      STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                           Genome sequence of an obligate intracellular pathogen of humans:
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Pred. No. 56;
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                                                                                                                                                                                                                     301 AA; 34076 MW; D82A7E0272CCC896 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09E427CA5CD5ACF2 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PHOSPHATIDYLSERINE DECARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                            01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBL_TaxID=83560;
                                            Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                   DB 2;
56;
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                                                                                                                                                                                                                                                     Score 27;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AE002274; AAF38954.1; -.
TIGR; TC0072; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003817; PS_Dcarbxylase.
Pfam; PF02666; PS_Dcarbxylase; 1.
                                                                                                                                                                                     InterPro; IPR003817; PS_Dcarbxylase.
Pfam; PF02666; PS_Dcarbxylase; 1.
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                               Science 282:754-759(1998).
EMBL; AE001340; AAC68294.1; -.
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85.7%;
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85.7%;
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                                 Chlamydia trachomatis.
                                                                                                                                                       Chlamydia trachomatis.
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Best Local Similarity
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Best Local Similarity
                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                          Complete proteome.
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SEQUENCE 301 AA
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|158 SMAIARL 164
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158 SMAIARL 164
                                                       NCBI_TaxID=813;
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                      PSDD OR CT699
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09PLM7
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RECENTER FORM N.A.

RECENTER FORM N.A.

RECENTER J. E. V. Palm C.J., Federspiel N.A., Kaul S.,

REDINE-21016719; PubMed=11130712;

REDINER R., Creasy T.H., Dewar K.,

REDINE R., Conn. L., Chonsy A.B., Conway A.R., Creasy T.H., Dewar K.,

REDINE C.J., Koo H.L., Rememetskala I., Kurtz D.B., Kwan A., Lam B.,

REDINE T.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

REDINE C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

REDINE R., Liu S.X., Liu Z.A., Luros J.S., Malti R., Mazziali A.,

REDINE R., Liu S.X., Liu Z.A., Luros J.S., Malti R., Mazziali A.,

REDINE R., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RESIDER R., Verser C.M., Verser R.W.,

RESIDE R., Verser C.M., Verser R.M.,

RESIDE R., Vers
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                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bevan M., Monfort A., Casacuberta E., Puigdomenech P., Hoheisel J.,
Mewes H.W., Mayer K.F.X., Schueller C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYOSCYAMINE 6-DIOXYGENASE HYDROXYLASE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 42.7 KDA PROTEIN.
T19P19.150 OR AT4G39760.
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329 AA.
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EMBL, AC079605, AAG50602.1; -.
InterPro; IPR002419; Fe_asc_oxidored.
InterPro; IPR002283; IPN_synth.
Pfam; PF00671; Fe_Asc_oxidored; 1.
PRINTS; PR00682; IPNSYNTHASE.
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Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26;
Pred. No.
                                                                                                                                                                                                                                            MEDLINE-97404404; Pubmed-9256491;
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002606; FAD_Synth.
Pfam; PF01687; FAD_Synth; 1.
ProDom; PD003662; FAD_Synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.78;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Labes 5; Conserve
                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-SB1003;
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205 NMSVARL 211
                                                                                                                                                                        NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SMSIARL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2810417D08RIK.
                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                          Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9CSEO;
                                   068069;
                   068069
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   690890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99310339; PubMed-10382966; Kawarabayasi Y., Hino Y., Horkawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Naqai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                  SEQUENCE FROM N.A.
Monfort A., Casacuberta E., Puigdomenech P., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aeropyrum pernix.
Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 27; DB 10; Length 369;
Pred. No. 68;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 1; Length 305;
Pred. No. 1e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
305AA LONG HYPOTHETICAL DIDP-4-DEHYDRORHAMNOSE REDUCTASE.
                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL02565; CAA18762.1; -.
EMBL; AL161595; CAB80639.1; -.
Mendel, 29837; Arath; 3427; 29837.
InterPro; IPROU1810; F-box.
InterPro; IPRO01798; Kelch.
 to the EMBL/GenBank/DDBJ databases.
                                                                                    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                al protein.
369 AA; 42660 MW; 900E2D1C01539684 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP000061; BAA80165.1; -.
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SEQUENCE 305 AA; 34301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   90.08;
71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 86.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                           SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                       Pfam; PF00646; F-box; 1.
Pfam; PF01344; Kelch; 1.
Submitted (APR-1998)
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
'... 5; Conserve
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                                                                                                                      SEQUENCE FROM N.A.
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|162 SMSVARI 168
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SMTVARL 105
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                                                                                                                                                                                                                                                                                                                                Hypothetical
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01-MAR-2001
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Q9YCT2 9

RESULT O9YCT2

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RESULT

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STRAIN-C57BL/63; TISSUE-EMBRYO;

KRAIN-C57BL/64; TISSUE-EMBRYO;

KRANAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishil Y.,

A Arakawa T., Hara A., Erkunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Fuzuno M., Panita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., Me Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,

Rusincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamico N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ruzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                              Vicek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.; "Sequence of a 189 kb segment of the chromosome of Rhodobacter capsulatus SB1003."; Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).

EMBL; AF010496; AAC16155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
01-806-1998 (TrEMBLrel. 07, Created)
01-80G-1998 (TrEMBLrel. 07, Last sequence update)
01-30T-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 33.2 KDA PROTEIN.
Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 307;
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307 AA; 33190 MW; 33CDFFED0FBFD6F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2810417D08RIK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; DB 2;
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Gaps

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RESULT Q90417

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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:3954899) (FRAGMENT).
Indoo sapiens (Hunan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                         Score 26; DB 4; Length 571;
Pred. No. 1.9e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.7%; Score 26; DB 3; Length 849; 100.0%; Pred. No. 2.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                         SEQUENCE FROM N.A.
TISSUE-SKIN, AND MELANOMA;
Strausberg ...
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC002929; AAH02929.1; -.
NON_TER
SEQUENCE 571 AA; 63247 MW; A1E7188792D7AE52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Urrestarazu L.A.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andre B., Urrestarazu L.A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X94607; CAA64304.1; -.
EMBL; Z73229; CAA97587.1; -.
EMBL; Z73230; CAA97589.1; -.
SGD; S0004047; YLR057W.
InterPro; IPR001382; Glyco_hydro_47.
Pfam; PF01522; Glyco_hydro_47.
ProDom; PD003239; Glyco_hydro_47; 1.
SEQUENCE 849 AA; 96996 MW; A6B87AC32936A0D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                              86.7%; SCUL.
71.4%; Pred. NO. 1...
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71,4%
..... 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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Best Local Similarity
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519 SMSLARI 525
                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                    1 SMSIARL 7
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MEDLINE-96009547; PubMed-7565671;
Jones B.B., Ohno C.K., Allenby G., Boffa M.B., Levin A.A.,
Grippo J.F., Petkoyich M.;
"New retinoid X receptor subtypes in zebra fish (Danio rerio)
differentially modulate transcription and do not bind 9-cis retinoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                  Gaps
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes: Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Nuclear protein; Receptor; Transcription regulation;
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0
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0
                                                                                                        Score 26; DB 11; Length 317;
Pred. No. 1.1e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.7%; Score 26; DB 13; Length 422; Best Local Similarity 71.4%; Pred. No. 1.4e+02; Matches 5; Conservative 2; Mismatches 0; Indels
EMBL; AK013101; BAB28647.1; -.
MGD; MGI:1917672; 2810417D08R1K.
1 1 1
SEQUENCE 317 AA; 34869 WW; 7D99ADD59C36BC82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 AA; 46732 MW; 6CCDBA3CE29C7238 CRC64
                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
RETINOID X RECEPTOR DELTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                422 AA
                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZETN; ZDB-GENE-990415-242; rxrd.
InterPro; IPRO00536; Hormone_rec_lig.
InterPro; IPRO01723; Strdhormone_receptor.
InterPro; IPRO01628; zf-C4.
Pfam; PPO0104; hormone_rec; 1.
Pfam; PF00105; zf-C4, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00430; HOLI; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                          Query Match 86.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative ;
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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186 SLSVARL 192
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                                                                                                                                                                                   1 SMSIARL 7
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Gaps

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Q9BU29;

09BU29 ID 09 AC 05 DT 01

Q9BU29

RESULT 10

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us-09-765-086-207.rspt

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Arabidopsis thaliana (Mouse-ear cress).
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POLYPROTEIN.
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Q85057;
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Q85057
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Ottenwaelder B., Obermaler B., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (JAN 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL136800; CAB66734.1; -.
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohara O.;
genes. XV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20039619; pubMed=10574462; Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code
                                                         Homo sapiens (Human).
Vertebrata; Euteleostomi;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4e+02;
2; Mismatches 0; Indels
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Pred. No. 4e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                          50B87F6FFF2A1088 CRC64;
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01.MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01.MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 134.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               PRT; 1209 AA.
                                                                                                                                                                              al protein.
1204 AA; 134345 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for large proteins in vitro.";
DNA Res. 6:337-345(1999).
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         KIAA1287 PROTEIN (FRAGMENT).
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                                     SEQUENCE FROM N.A.
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1073 SLSVARL 1079
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                                               DKFZP434H1220.
                                                                                                                                                                              Hypothetical
SEQUENCE 12
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Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mawes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cassidy B., Sherwood J.L., Nelson R.S.; "Cloning of the capsid protein gene from a blotch isolate of peanut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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MEDLINE-94358761; PubMed=8077957;
Gunasinghe U.B., Flasinski S., Nelson R.S., Cassidy B.G.;
"Nucleotide sequence and genome organization of peanut stripe potyvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%; Score 26; DB 10; Length 1216; ilarity 71.4%; Pred. No. 4.1e+02; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC07138; AAD22648.1; -
EMBL, AL161493; CAB80679.1; -
InterPro; IPR001680; WD40.
R Fām; PR00400; WD40; 7.
SMART; SM00320; WD40; 7.
R PROSITE; PS50082; WD_REPEATS_1; UNKNOWN_3.
R PROSITE; PS50082; WD_REPEATS_2; 1.
R PROSITE; PS5094; WD_REPEATS_2; 1.
R PROSITE; PS5094; WD_REPEATS_REGION; 1.
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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MEDLINE=93168029; PubMed=7916587;
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SEQUENCE OF 2854-3222 FROM N.A.
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Arch. Virol. 128:287-297(1993).
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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NCBI_TaxID=28353;
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| SLSVARL 607
                                                                                                                                                    NCBI_TaxID=3702;
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1300 1933 CI.

1934 1986 6K2.

2177 2419 NIA-VPG.

2420 2935 NIB.

2936 3222 AA; 365723 MW; 96E3CE717D634B50 CRC64;
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InterPro; IPR001505; Helicase_C.
InterPro; IPR001505; Peptidase_C4.
InterPro; IPR001505; Peptidase_C6.
InterPro; IPR001502; Poty_coat.
InterPro; IPR001204; Poty_P1.
InterPro; IPR001204; Trypsin.
InterPro; IPR001204; Irypsin.
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6 КІ.
J. Gen. Virol. 75:2519-2525(1994).
                                                                                                                 SEQUENCE FROM N.A.
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Search completed: May 8, 2002, 07:20:16 Job time: 144 sec

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GenCore version 4.5 . Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 8, 2002, 07:20:33 ; Search time 12.86 Seconds (without alignments) 19.958 Million cell updates/sec Run on:

US-09-765-086-207 30 1 SMSIARL 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P56346 chlorella v	mesos		mus m	P77439 escherichia	P02369 escherichia	P51295 porphyra pu	P26161 rhodobacter					P42786 neisseria g	Q9juvl neisseria m	Q9jzr6 neisseria m	027262 methanobact		-	P93768 nicotiana t		O51522 borrelia bu	-	Q09263 caenorhabdi				Q04668 leishmania		P27009 octopus dof	P27014 octopus vul	Q25626 octopus vul	114	Q56301 thermococcu
SUMMAKIES		ID	MIND_CHLVU	MIND_MESVI	KHL1_HUMAN	KHL1_MOUSE	YPDD_ECOLI	RS13_ECOLI	RR13_PORPU	YPU5_RHOCA	RS7_SYNP6	ADH_DROPI	YIAJ_HAEIN	YYBE_BACSU	PIP_NEIGO	PIP_NEIMA	PIP_NEIMB	YB94_METTH	GSPF_XANCP	PS31_ARATH	PSD3_TOBAC	CALR_RAT	PYRG_BORBU	VIB4_AGRT9	YQD3_CAEEL	DPOM_PODAN	CHAO_DROME	RPB1_SCHPO	KPYK_LEIBR	DPA6_BPR69	SC1_OCTDO	SC2_OCTVU	SC3_OCTVU	YLP4_ZYMMO	KPYK_THELI
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æ		Match	86.7	86.7	86.7	86.7	86.7	83.3	83.3	83.3	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	76.7	76.7	76.7		76.7	٠	76.7
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RESULT 2 MIND_MESVI

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053345 P13714 018079 056186 026105 028105 P33770 067259 0953K3 0953K4 09616 P30615	AA. (e) MIND. MAN. (ebouxiophyceae; The M., Ito M., Ito M., Ito M., Ito M., Ito M., Ito M.) Ancelast genome force of qenes poss	2(1997). RECT PLACEMENT O Y. MIND SUBFAMIL produced throug attics and the here are no res as its content d. Usage by a e http://www.isb	Chloroplast. TIAL). 5AE4AEC7 CRC64; DB 1; Length 282; 14; hes 0; Indels 0
NUDC_MYCTU LDH_BACSU YXT1_CAEEL WUIM_PECMA YG59_SYNY3 YL78_ARCFU HEMF_RHOSH HEMF_RHOSH HEMF_RHOSH HTHIC_AQUAE SELA_EUBAC MOTD_RHIME FKH1_YEAST	T. 1 CHLVU CHLVU STANDARD; PRT; 282 AA. P56346; 15-JUL-1998 (Rel. 36, Created) 20-AUG-2001 (Rel. 40, Last sequence update) PUTALIVE SEPTUM SITE-DETERMINING PROTEIN MIND AND. Chlorella vulgaris. Chlorellaces; Chlorella. Chlorellaceae; Chlorella. ROBI_TAXID=3077; Il SEQUENCE FROM N.A. STRAIN=IAM C-27 / TAMIYA; WAGBLUE T, Nadaahima K., Sugita M., Wadasugi T., Nadaahima K., Tsudzuki T., Suzuk Inamura A., Yoshinaga K., Sugiura M.; Inamura A., Yoshinaga K., Sugiura M.; Inamura A., Yoshinaga K., Sugiura M.; Inamure A., Yoshinaga K., Sugiura M.; Inamure A., Yoshinaga K., Sugiura M.; Inamura A., Yoshinaga K., Sugiura M.;	st division."; "U.S.A. 94.5967-5972(1997 "EQUIRED FOR THE CORRECT IS INCLARITY) GS TO THE PARA FAMILY. MIN STRUCT IS COPYIGHT. It is produced to the produce of Bioinformatics matics Institute. There is not removed. Us tement is not removed. Us icense agreement (See httlicensee agreement).	P-binding; ATP (POTEN V; 94010DD4 Score 26; Pred. No. 0; Mismatc
7 3323 1 3320 1 3320 1 3320 1 1 3320 1 1 2 3320 1 1 2 3320 1 2 332	CHLVU CHLVU STANDARD; P56346; 15-701-1998 (Rel. 36, Created) 15-701-1998 (Rel. 36, Last seq 20-AUG-2001 (Rel. 40, Last ann PUTATIVE SEPTUM SITE-DETERMINI CHIO. Chlorella vulgaris. Chloroplast. SEGUENCE FROM N.A. STERIN-IAM C-27 / TAMIYA; S	inloroplast division.; ATPASE REQUIRED FOR THE SITE (BY SIMILARITY). YY. BELONGS TO THE PARA FA NOT entry is copyright. It Swiss Institute of Bioinf Bioinformatics Institute. Profit institute institute. Profit institute is at rement is not rem lires a license agreement mail to licenseeds.	951.1 ParA.1 1. 1013 1013 86.78 86.78 100.0
23 23 23 24 25 25 26 27 26 27 27 27 27 27 27 27 27 27 27 27 27 27	T 1 CHLVU F56346; P56346; 15-JUL-1998 (Rel. 15-JUL-1998 (Rel. 20-AUG-2001 (Rel. MIND. Chlorella vulgaris Chloroplast. Chloroplast. Chloroplast. Chloroplast. SEPURATYORS (Chloroplast. Chloroplast. Chloroplast. SCHARTYORS (Chloroplast.) Chloroplast. Chloroplast. SCHARTYORS (Chloroplast.) SCHARTYORS (Chloroplast.) Chloroplast. Chloroplast. SCHARTYORS (Chloroplast.) SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-IAM C-27 / WEDLINE-97303241; WARASUGI T., NAGRA TSUGARLINE-97303241; WARASUGI T., NAGRA TSUGARLINE-9730341; WARASUGI T., NAGRA TSUGARLINE-9730341; WARASUGI T., NAGRA TSUGARLINE-9730341; WARASUGI T., NAGRA TSUGARLINE-9730341; WARASUGI T., NAGRA TSUGARLINE-973041; WARASUGI T., NAGRA TSUGAR	involved in chloropo Proc. Natl. Acad. Sc. - FUNCTION: ATPASI DIVISION SITE (SIMILARITY: BELG This SWISS-PROT entr Detween the Swiss of the European Bioinf use by non-profit use by non-profit use by non-profit entries requires a entities requires a or send an email to	UULD84; UPR00 00991; ision; 282, 282, Similar 6; Con 6; Con
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MIM; 605332;
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Q9JI74;
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KHL1_MOUSE
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MEDLINE=20150907; PubMed=10688199;
Lemieux C., Otis C., Turmel M.;
Ancestral chloroplast genome in Mesostigma viride reveals an early branch of green plant evolution.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-1- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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Koob M.D., Nemes J.P., Benzow K.A.;
"The SCA8 transcript is an antisense RNA to a brain-specific
transcript encoding a novel actin-binding protein (KLHLI).";
Hum. Mol. Genet. 9:1543-1551(2000).
                                                                                                                                                                   Chloropíast.
Eukaryota: Viridiplantae; Streptophyta; Mesostigmatophyceae;
Mesostigmatales; Mesostigmataceae; Mesostigma.
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25D8B8FB2258E3F9 CRC64;
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                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND
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  286 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                        branch of green plant evolution.";
Nature 403:649-652(2000).
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MEDLINE=20277482; PubMed=10819331;
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286 AA; 31627 MW;
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Best Local Similarity 100.
Matches 6; Conservative
  STANDARD;
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                                                                                                                                                  Mesostigma viride.
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40 MSIARL 45
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Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 7:143-150(2000).
                                                                                                                                                                                    Ray M.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
THE BRAIN CELLS.
THE BRAIN CELLS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                             -i-TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-i-SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
-i-SIMILARITY: CONTAINS 6 KELCH REPEATS.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KELGH-LIKE PROTEIN 1.
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SER-RICH.
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KELCH 3.
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KELCH 5.
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EMBL; AB040923; BAA96014.1; ALT_INIT.
EMBL; AL353738; CAC16128.1; -.
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SEQUENCE FROM N.A.
MEDLINE-20347694; Pubmed-10888605;
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Pfam; PF01344; Kelch; 6.
PRINTS; PR00501; KELCHREPEAT.
SWART; SM0225; BTB; 1.
PROSTTE; PS50097; BTB; 1.
Cytoskeleton; Actin-binding; Re
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SEQUENCE OF 179-409 FROM N.A.
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InterPro; IPR001798; Kelch.
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601
649
701
748 AA;
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92129 MW;
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Similarity 85.7%;
6; Conservative 1
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298
831 AA;
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Best Local Similarity
Matches 6; Conserv
    SEQUENCE FROM N.A.
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757 SISIARL 763
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                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Koob M.D., Nemes J.P., Benzow K.A.;
"The SCA0 transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI).";
Hum. Mol. Genet. 9:1543-1551(2000).
-i- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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STRAIN=KIZ ' MG1652;
STRAIN=KIZ ' MG1657;
PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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30-MAY-2000 (Rel. 39, Last sequence update)
20-MAG-2001 (Rel. 40, Last annotation update)
PUTATIVE PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE YPDD
(EC 2.7.3.9) (PHOSPHOTRANSFERASE SYSTEM, ENZYME I).
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Science 277:1453-1474(1997).
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KELCH 2.
KELCH 3.
KELCH 4.
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KELCH 5.
                                                                    THE BRAIN CELLS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
-!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
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SER-RICH.
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InterPro; IPR000210; BTB_POZ.
InterPro; IPR001798; Kelch.
Pfam; PF00151; BTB; 1.
Pfam; PF01344; Kelch; 6.
PRINTS; PR00501; KELCHREPEAT.
SMART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
Cytoskeleton; Actin-binding; Repe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82932 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Best Local Similarity
6; Conserve
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510
558
604
652
704
751 AA;
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P77439;
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REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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YPDD_ECOLI
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                                               A Tanamator Y., Albah H., Baba T., Hayashi K., Inada T., Isono K.,
A Tanamator Y., Albah H., Baba T., Makino K., Miki T., Mitsuhashi N.,
A Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
A Mizobuchi K., Mori H., Makade S., Makamura Y., Mashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
Yamagata S., Horiuchi T.;
Tanagata S., Horiuchi T.;
Toonstruction of a contiguous 87-kb sequence of the Escherichia coli
T. Construction of a contiguous 87-kb sequence of the Escherichia coli
T. T. Seguence features.";
DNA Res. 4:91-13119197

C. I. SALALYITC ACTIVITY: PHOSPHOHISTIDINE
PYRUVATE + PROTEIN N-PHOSPHOHISTIDINE

C. I. SUBLELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
C. I. SIMILARITY: CONTAINS I HPR DOMAIN.
C. I. SIMILARITY: CONTAINS I HPR EIJA DOMAIN.
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Escherichia.
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PHOSPHORYLATION (BY SIMILARITY).
B9F3E3B6D4EAB597 CRC64;
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Pred. No. 45;
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21-JUL-1986 (Rel. 01, Last sequence update)
20-AUC-2001 (Rel. 40, Last annotation update)
30S RIDOSOWAL PROTEIN S13.
BSSM OR B3298.
Escherichia coli.
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Mismatches
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EMBL, D90668; BAA16253.1; -...
EcoGene; EG14151; ypdb.
InterPro; IPR00121; PFE_utilizers.
InterPro; IPR002178; PTS_EIIA_2.
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MEDLINE=97349980; PubMed=9205837;
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SEQUENCE FROM N.A.
MEDLINE-85242076; PubMed-2989779;
Bedwell D.M., Davis G.R., Gosink M., Post L.E., Nomura M., Kestler H.,
Zengel J.M., Lindahl L.;
"Nucleotide sequence of the alpha ribosomal protein operon of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MASS SPECTROMETRY.

MEDLINE=99196679; PubMed=10094780;

Arnold R.J., Reilly J. P.;

And R.J., Reilly J. P.;

"Observation of Escherichia coli ribosomal proteins and their posttranslational modifications by mass spectrometry.";

Anal. Biochem. 269:105-112(1999).

I PINCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE INITIATION OF TRANSLATION.

INITIATION OF TRANSLATION.

-!- MASS SPECTROMETRY: MW=12968.1; METHOD=MALDI.

-!- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-35 FROM N.A. MEDITINE-62025589; Pubmed-6793240; Miura A., Krueger J.H., Itoh S., de Boer H.A., Nomura M.; Growth-rate-dependent regulation of ribosome synthesis in E. coli: expression of the lacz and galk genes fused to ribosomal promoters.";
                                                                                                                                                                                                                                                                                                                                                                                                                         for the alpha ribosomal protein
                                                                                                                                      MEDIJNE-97426617: PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                        Lindemann H., Wittmann-Liebold B.; "Primary structure of protein S13 from the small subunit of Escherichia coli ribosomes."; Hoppe-Scyler's Z. Physiol. Chem. 358:843-863(1977).
                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12968 MW; 3277C328EBD0D3D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-35 FROM N.A.
MEDLINE-80182128; PubMed=6154696;
Post L.E., Arfsten A.E., Davis G.R., Nomura M.;
"DNA sequence of the promoter region for the alpoperon in Escherichia coli.";
J. Biol. Chem. 255:4653-4659(1980).
                                                                                       Nucleic Acids Res. 13:3891-3903(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein; Complete proteome.
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Interpro; IPR001892; Ribosomal_S13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001363; Ribosomal_S13; 1. PROSITE; PS00646; RIBOSOMAL_S13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M12432; AAA83903.1; -.
EMBL; U18997; AAA58093.1; -.
EMBL; AE000407; AAC76323.1; -.
EMBL; X02543; CAA26392.1; -.
EMBL; M10213; AAA72457.1; -.
PIR; A23807; R3EC13.
                                                                                                                                                                                                                                                                                         MEDLINE-77248097; PubMed-330375;
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                                                                                                                    SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                         Escherichia coli.";
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant Mol. Biol. Rep. 13:333-335(1995).
-!- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE INTIGATION OF TRANSLATION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reith M.E., Munholland J.; "Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
MYPOTHETICAL 23.7 Kap PROTEIN IN PUHA 5'REGION (ORF214) (PROTEIN
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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Length 117;
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                                                     Indels
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     DB 1;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
CHLOROPLAST 30S RIBOSOMAL PROTEIN S13.
     Score 25; DB ]
Pred. No. 9.9;
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InterPro; IPR001892; Ribosomal_S13.
Probom; PP00416; Ribosomal_S13; 1.
Probom; PD001363; Ribosomal_S13; 1.
PROSITE; PS00646; RIBOSOMAL_S13; 1.
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83.3%;
85.7%;
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                                                        Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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     Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphyra purpurea.
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ID YPUS_RHOCA
AC P26161;
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P51295;
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PIR; S04428; S04428.
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24 SMMVARL 30
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                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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Meng B.Y. Shinozaki K., Sugiura M.;
Meng B.Y. Shinozaki K., Sugiura M.;
"Genes for the ribosomal proteins S12 and S7 and elongation factors
EF-G and EF-Tu of the cyanobacterium, Anacystis nidulans: structural
homology between 16S rRNA and S7 mRNA.";
Mol. Gen. Genet. 216:25-30(1989).
-!- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                       MEDLINE-84259352; PubMed-6744416; Youvan D.C., Bylina E.J., Alberti M., Begusch H., Hearst J.E.; Mucleotide and deduced polypeptide sequences of the photosynthetic reaction-center, B870 antenna, and flanking polypeptides from R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                            Burke D.H., Alberti M., Armstrong G.A., Hearst J.E.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Photosynthesis; Hypothetical protein.
SEQUENCE 214 AA; 23658 MW; BC4B773AF6631FA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
30S RIBOSOMAL PROPEIN S7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.3%; Score 25; DB Best Local Similarity 71.4%; Pred. No. 19; Matches 5; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 211165; CAA77519.1; -
EMBL; KOIL33; -; OT_ANNOTATED_CDS.
PIR; C28988; C28988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X17442; CAA35494.1; -.
                                                                                                                                                                SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                         capsulata.";
Cell 37:949-957(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16S RIBOSOMAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                   SEQUENCE FROM N.A.
                 CBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 SMSLAKL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SMSIARL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RS7_SYNP6
P18661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RS7_SYNP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila picticornis (Fruit fly) (Idiomyla picticornis).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - CATALYTIC ACTIVITY: ALCOHOL + NAD(+) = ALDEHYDE OR KETONE + NADH. -! - SUBUNIT: HOMODIMER. -! - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-91163323; PubMed-2002765; MEDLINE-91163323: PubMed-2002765; Rowan R.G., Hunt J.A.; Rates of DNA change and phylogeny from the DNA sequences of the alcohol dehydrogenase gene for five closely related species of
                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                        Length 156;
                                                                                                                                                                                                                                                                                                                                           Indels
HSSP; P22744; 1HUS.
InterPro: IPR00235; Ribosomal_S7.
Pfam: PF00177; Ribosomal_S7: 1.
ProDom: PD000817; Ribosomal_S7: 1.
PROSITE; PS000052; RIBOSOMAL_S7: 1.
Ribosomal protein; rRNA binding.
SEQUENCE 156 AA; 17734 MW; 240FE99581CADCCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12CDAAB491E3505B CRC64;
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NAD (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                        DB 1;
25;
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01-MAY-1992 (Rel. 22, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
ALCOHOL DEHYDROGENASE (EC 1.1.1.1).
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                        Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR002198; ADH_Short.
InterPro; IPR003193; Adh_Short_C.
InterPro; IPR000205; NAD_binding.
Pfam; PF00106; adh_Short; 1.
Pfam; PF00663; adh_Short_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PRO0080; SUPENAILY.
PRINTS: PRO1167; INSAHFAMILY.
PRINTS: PRO1168; ALCHUDRGNASE.
PROSITE: PRO1061; ADH_SHORT; 1.
OXIGOTEGUCTASE; NAD.
INIT_MET 0 0 0 BY SIN P_BIND 9 32 NAD.
ACT_SITE 150 150 BY SEQUENCE 253 AA; 27437 MW; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Biol. Evol. 8:49-70(1991).
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                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                        80.0%;
71.4%;
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                                                                                                                                                                                                                                                                           Query Match 80.0
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hawaiian Drosophila.
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PRT;

STANDARD;

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PIP_NEIGO
P42786;
  YYBE_BACSU
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SEQUENCE
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  HDDDH BERNER BER
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=RD, /KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MERLIANDE R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback Tr., Hanna M.C., Nguyen D.T., Sauddek D.M., Brandon R.C., Ghin L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Ghehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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-!- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL REGULATORS. STRONG, TO E.COLI YIAJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophius.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD002768; HTH_IC1R; 1.
SMART; SM0346; HTH_ICLR; 1.
PROSITE; PS01051; HTH_ICLR FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 85.7%; Pred. No. 45; 6; Conservative 0; Mismatches 1; Indels
Score 24; DB 1; Length 253;
Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 H-T-H MOTIF (POTENTIAL).
30580 MW; AAAF3080ED39EA14 CRC64;
                                                                                                                                                                                                                                                                        YIAJ_HAEIN STANDARD; PRT; 268 AA. P44996; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 20-ANG-2001 (Rel. 40, Last annotation update) HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI1032.
                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000285; HTH_ICLR.
Pfam; PF01614; ICLR; 1.
80.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32784; AAC22692.1; -.
                                                 5; Conservative
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               Best_Local Similarity
Matches 5; Conserv
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Best Local Similarity
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                                                                                                                            :||||:|
161 TMSIAKL 167
                                                                                             1 SMSIARL 7
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  Query Match
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YYBE_BACSU
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROLINE IMINOPEPTIDASE (EC 3.4.11.5) (PIP) (PROLYL AMINOPEPTIDASE)
                                                                                                                                                                                                                                                                                                                                                                  Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
DNA Res. 1:1-14(1994).
-:- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 80.0%; Score 24; DB 1; Length 278; Best Local Similarity 85.7%; Pred. No. 47; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 H-T-H MOTIF (BY SIMILARITY).
31406 MW; 0F7750102F0FC0F7 CRC64;
                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
01-ocr-1994 (Rel. 30, Created)
01-ocr-1994 (Rel. 30, Last sequence update)
02-bdG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YYBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
STRAIN-MS11 / MSO1-1X;
                                                                                                                                                                                                                                                                                                                  STRAIN=168;
MEDLINE=96051385; PubMed=7584024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95020651; PubMed=7934933;
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InterPro; IPR000847; HTH_LysR.
Pfam; PF00126; HTH_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D26185; BAA05198.1; -. EMBL; Z99124; CAB16104.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 AA;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                             NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | ||||||
| 9 SRSIARL 25
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Matches
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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09JUV1;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROLINE IMINOPEPTIDASE (EC 3.4.11.5) (PIP) (PROLYL AMINOPEPTIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIM-22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE-2022556; pubMed-10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd idagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
FUNCTION: HYDROLYSES PEPTIDES HAVING THE STRUCTURE PRO-Y-Z TO YIELD FREE PROLINE. ALSO HYDROLYSES THE DIPEPTIDE PRO-GLY. CATALYTIC ACTIVITY: RELEASE OF A N-TERMINAL PROLINE FROM A
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                                                                                                                                                                                                                                                                                       BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
DOE7AEBA908A1AE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                   1; Length 310;
                                                                                                                                                                                                                                                                             NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S33.
                                    PEPTIDE.
SUBCELULAR LOCATION: CYTOPLASMIC (PROBABLE).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S33.
                                                                                                                                                                                                  InterPro; IPR000073; Abhydrolase.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR002410; Pro_amnoPTase.
                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Score 24; DB
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                    Pfan; PF00561; abhydrolase; 1.
PRINTS; PR00793; PROAMNOPTASE.
Hydrolase; Aminopeptidase.
                                                                                                                                                                                                                                                                                                               34791 MW;
                                                                                                                                                                              EMBL; Z25461; CAA80948.1; -.
                                                                                                                                                                                                                                                                                                                                                 80.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                               310 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=65699;
                                                                                                                                                                                           MEROPS; S33.001;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-MC58 / SEROGROUP B;

MEDLINE-2017755; PubMed-10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 287:1809-1815(2000).
-!- FUNCTION: SPECIFICALLY CATALYZES THE REMOVAL OF N-TERMINAL PROLINE RESIDUES FROM PEPTIDES (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: RELEASE OF A N-TERMINAL PROLINE FROM A
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Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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Co-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROLINE IMINOPEPTIDASE (EC 3.4.11.5) (PIP) (PROLYL AMINOPEPTIDASE)
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9F888B54135478A1 CRC64;
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BY SIMILARITY.
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InterPro; IPR000039; AB_hydrolase.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000639; Epox_hydrlse.
InterPro; IPR000439; Epox_hydrlse.
InterPro; IPR000419; Ext_lip_thioset_actsite.
InterPro; IPR000410; Pro_amnoPrase.
Pfam; PF00561; abhydrolase; I.
PRINTS; PR00111; ABHYDROLASE.
PRINTS; PR00112; EPOXHYDRLASE.
PRINTS; PR00193; PROAMNOPTASE.
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Bacteria, Proteobacteria, beta subdiv
NCBI_TaxID-491;
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71.4%;
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ACT_SITE
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or send an email to license@isb-sib.ch).

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           EMBL; AE002444; AAF41334.1; -.

R TIGR; MB0027; -.

R InterPro; IPR003089; AB_hydrolase.
R InterPro; IPR000073; Abhydrolase.
R InterPro; IPR000073; Abhydrolase.
R InterPro; IPR000379; Epox_hydrlse.
R InterPro; IPR000379; Epox_hydrlse.
R Pfam; PF00561; abhydrolase; 1.
R PRINTS; PR00111; ABHYDROLASE.
R PRINTS; PR00711; ABHYDROLASE.
R PRINTS; PR00712; EPOXHYDRIASE.
R PRINTS; PR00712; EPOXHYDRIASE.
R PRINTS; PR00793; PROANNOPTASE.
R PAT_SITE 260 BY SIMILARITY.
T ACT_SITE 260 BY SIMILARITY.
T ACT_SITE 287 287 PROTON DONOR (BY SIMILARITY).
SEQUENCE 310 AA; 34956 WW; 9F883415B1C7B4A2 CRC64;
                                                                                                                                                                                                                                                                                                                               Query Match 80.0%; Score 24; DB 1; Length 310; Best Local Similarity 71.4%; Pred. No. 53; Matches 5; Conservative 2; Mismatches 0; Indels
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217 SLAIARL 223
qq
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Search completed: May 8, 2002, 07:20:34 Job time: 162 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

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8, 2002, 07:19:31; Search time 22.68 Seconds (without alignments) 23.511 Million cell updates/sec

US-09-765-086-207 30 1 SMSIARL 7 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable phosphati	phosphatidylserine	probable hyoscyami	hypothetical prote	cell division inhi	probable dTDP-4-de	conserved hypothet	retinoid X recepto	hypothetical prote	hypothetical prote	Д	hypothetical prote	hypothetical prote	a	30S ribosomal subu	ribosomal protein	hypothetical prote	hypothetical prote	٠			hypothetical prote	¥	hypothetical prote	hypothetical prote	ribosomal protein	alcohol dehydrogen	hypothetical prote	hypothetical prote
SUMMARIES	ID	D81745	E71482	G86472	T05013	T07303	G72588	T03502	150516	A85881	D65012	S61631	H85023	G85926	R3EC13	G85994	S73216	D86170	S17807	T38115	C83338	S76046	T47405	T00077	T42264	G83348	S04428	B23724	D71945	D64165
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DNA processing cha	transcription regu hypothetical prote	transcription regu	prolyl aminopeptid	probable prolyl am	proline iminopepti	hypothetical prote	hypothetical prote	acetylpolyamine am	hypothetical prote	xpsF protein - Xan	xpsF protein - Xan	calcitonin recepto	calcitonin recepto	protein 21D7 - com
E64561	S65992 T32333	F82446	S39592	F81878	B81141	F72575	A83708	C69026	T01839	S17938	T12057	A37430	S33746	T02207
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30	31 32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 191745 192046 192046 192057 192057 1920
 Nucleic Acids Nes. 20, 1997-1409, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Reference number: A81500; MUID:20150255 A;Accession: D81745 A;Status: preliminary A;Molecule type: DNA
A; Residues: 1-301 <tet> A; Residues: 1-301 <tet> A; Cross references: GB: AE00215; GB: AE002160; NID: g7190108; PIDN: AAF38954.1; PID: g719 A; Experimental source: strain Nigg (MoPn) C; Generics: A; Gene: TC0072</tet></tet>
 _ 0
 Query Match 90.0%; Score 27; DB 2; Length 301; Best Local Similarity 85.7%; Pred. No. 22; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

||:|||| |158 SMAIARL 164 1 SMSIARL 7 g ò

~ RESULT

E71482
phosphatidylserine decarboxylase (EC 4.1.1.65) precursor - Chlamydia trachomatis (ser C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 28-Jul-2000
C;Accession: E71482
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t A;Reference number: A71570; MUID:99000809

A; Accession: E71482
A; Status: preliminary
A; Status: 1-301 < ARN>
A; Cross-references: GB: AE001340; GB: AE001273; NID: g3329147; PIDN: AAC68294.1; PID: g332
A; Experimental source: serotype D, strain UW-3/Cx
C; Genetics:
C; Genetics:
C; Genetics:
C; Superfamily: Escherichia coli phosphatidylserine decarboxylase
C; Keywords: carbon-carbon lyase; carboxy-lyase

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162 SMSVARI 168

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Length 301;

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Accession inhibitor - Chlorella vulgaris chloroplast
C; Species: chloroplast Chlorella vulgaris
C; Species: chloroplast Chlorella vulgaris
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C; Date: 17-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C; Accession: T707303
B; Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Na Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A; Title: Complete nucleotide sequence of the chloroplast genome from the green alga C A; Reference number: 215985; MUID: 97303241
A; Accession: T07303
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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C;Species: Aeropyrum pernix
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: G72588
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res 6, 83-101, 1999
A;Tile: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Accession: G72588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-282 <WAK>
A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57951.1; PID:g2224467
C;Genetics:
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C;Species: Rhodobacter capsulatus
C;Species: Thodobacter capsulatus
C;Accession: T03502
R;Vicek, C;Pacess, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 282;
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38;
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C, Superfamily: dTDP-dihydrostreptose synthase
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C;Superfamily: cell division inhibitor minD
C;Keywords: chloroplast
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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99 SMTVARL 105
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                                                                                                                                                                                                                                                                                                                                                                                        probable hyoscyamine 6-dioxygenase hydroxylase [imported] - Arabidopsis thaliana c'Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G86472
C;Accession: G96472
C;Accession: G86472
C;Accession: Garage Accession: Garage
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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A; Molecule type: DNA
A; Residues: 1-369 < ABEV>
A; Cross-references: EMBL:AL022605
A; Experimental source: cultivar Columbia; BAC clone T19919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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Pred. No. 24;
1; Mismatches
   Score 27; DB 2;
Pred. No. 22;
1; Mismatches
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Pred. No. 27;
2; Mismatches
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A;Note: T19P19.150
C;Superfamily: caffeoyl-CoA 3-0-methyltransferase
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       90.0%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                               6; Conservative
Query Match
Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-329 <STO>
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| 150 SMAIARL 156
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| 158 SMAIARL 164
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Length 831;

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C; Species: Escherichia coli

C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999

C; Accession: D65012

R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Accession: D65012

A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Molecule type: DNA
A;Residues: 1-831 <BLAT>
A;Crossidues: 1-831 <BLAT>
A;Crossidues: GB:AEO00326; GB:U00096; NID:g1788718; PIDN:AAC75442.1; PID:g17887
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: phosphotransferase system enzyme I homology
F;118-670/Domain: phosphotransferase system enzyme I homology <PT1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YLR057w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L2153
C;Species: Saccharomyces cerevisiae
C;Dapeide: Saccharomyces cerevisiae
C;Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 21-Nov-1997
C;Accession: S61631; 864885
R;Urrestarazu, L.A.
submitted to the EMBL Data Library, December 1995
A;Reference number: S61618
A;Reference number: S61618
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A; Residues: 1-849 < URR>
A; Cross-references: EMBL:X94607; NID:g1181264; PID:e217771; PID:g1181278
A; Cross-references: EMBL:X94607; NID:g1181264; PID:e217771; PID:g1181278
B; Andre, B.; Urrestarazu, L.A.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64872
A; Accession: S64885
A; Molecule type: DNA
A; Residues: 1-849 < AND>
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illarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein b2383 - Escherichia coli (strain K-12)
Score 26; DB 2; Ler
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 2; Ler
Pred. No. 1.2e+02;
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C;Keywords: transmembrane protein
F;16-32/Domain: transmembrane #status predicted <TMM>
                                                                                                       1; Mismatches
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85.7%;
                                 86.7%;
ilarity 85.7%;
Conservative
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conser
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757 SISIARE 763
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757 SISIARL 763
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C;Species: Brachydanio retio (zebra fish)
C;Species: Brachydanio retio (zebra fish)
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 20-Sep-1999
C;Accession: 156016
R;Jones, B.B.; Ohno, C.K.; Allenby, G.; Boffa, M.B.; Levin, A.A.; Grippo, J.F.; Petkovic
R;Jones, B.B.; Ohno, C.K.; Allenby, G.; Boffa, M.B.; Levin, A.A.; Grippo, J.F.; Petkovic
Mol. Cell. Biol. 15, 5226-5234, 1995
A;Title: New retinoid X receptor subtypes in zebra fish (Danio retio) differentially mod
A;Reference number: A57301; MUID:96009547
A;Reference number: A57301; MUID:96009547
A;Reference number: A57301
A;Molecule type: mRNA
A;Residues: 1-422
A;Molecule type: MRNA
A;Residues: 1-424
A;Residues: 
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hypothetical protein Z3648 [imported] - Escherichia coli (strain O157:H7)

C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Bacherichia coli
C;Accession: A85881

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Reference number: A85881

A;Accession: A85881

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-831 <Cross-references: GB:AE005174; NID:g12516757; PIDN:AAG57509.1; GSPDB:GN00145; UWGP:Z36

A;Experimental source: strain O157:H7, substrain EDL933
                             A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A;Reference number: 214955; WUID:97404404
                                                              A; Reference number: 214955; MULD: >/4v4*v*
A; Accession: T03502
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-307 <VLC>
A; Residues: 1-307 <VLC>
C; Genetics: EMBL: AF010496; NID: 93128256; PIDN: AAC16155.1; PID: 93128303
C; Genetics: A; Map position: 1
C; Superfamily: conserved hypothetical protein HI0963
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Pred. No. 41;
2; Mismatches
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71.4%; Pred. No. 58;
Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 86.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative 5
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205 NMSVARL 211
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53 SMSVSRL 59
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C.Species: Escherichia coli

C.Species: Escherichia coli

C.Apecies: Escherichia coli

C.Abet: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C.Accession: G85994

R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A.Reference number: A85480; MUID:21074935; PMID:11206551

A.Accession: G85994

A.Status: preliminary

A.Status: preliminary

A.Residues: 1-118 <STO>

A.Residues: 1-118 <STO>

A.Coss-references: GB:AE005174; NID:q12517927; PIDN:AAG58419.1; GSPDB:GN00145; UWGP:

A.Experimental source: strain 0157:H7, substrain EDL933

C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain K
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau. B.; Shao, Y.
Science 277, 1453-1464, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Accession: E6512
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: rpsM
A;Map position: 73 min
A;Start codon: GTG
C;Complex: the ribosome is composed of the large (50S) and small (30S) subunit; the l
S rRNA and 22 distinct proteins
C;Complex: small subunit ribosomal proteins: S1 (PIR:R3EC1), S2 (PIR:R3EC2), S3 (PIR:
R3EC10), S11 (PIR:R3EC11), S12 (PIR:R3EC12), S13 (PIR:R3EC13), S14 (PIR:R3EC14), S15
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-118 <BLAT>
A; Cross-references: GB:AE000407; GB:U00096; NID:g2367211; PIDN:AAC76323.1; PID:g17896
A; Experimental source: strain K-12, substrain MG1655
R; Arnold, R.J.; Reilly, J.P.
Anal. Biochem. 269, 105-112, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Observation of Escherichia coli ribosomal proteins and their posttranslation A;Reference number: A59071; MUID:99196679
A;Contents: annotation; mass spectrographic analysis
A;Note: mass spectrographic analysis of post-translational modifications; any acid la C;Genetics:
                         A;Cross-references: GB:X02543; NID:g42795; PIDN:CAA26392.1; PID:g581217
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
R;Lindemann, H.; Wittmann-Liebold, B.
Hoppe-Seyler's Z. Physiol. Chem. 358, 843-863, 1977
A;Title: Primary structure of protein S13 from the small subunit of Escherichia coli
A;Reference number: A02731; MUID:77248097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30S ribosomal subunit protein S13 [imported] - Escherichia coli (strain O157:H7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Pathway: protein biosynthesis
C; Superfamily: Escherichia coli ribosomal protein S13
C; Keywords: protein biosynthesis; ribosome
F; 2-118/Product: ribosomal protein S13 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 1; Length 118;
Pred. No. 28;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 2-118 <LIN>
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    A; Molecule type: DNA
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74 SMSIKRL 80
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: 685926
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <STO>
A;Residues: 1-98 <STO>
A;Cross-references: GB:AE005174; NID:912517228; PIDN:AAG57875.1; GSPDB:GN00145; UWGP:24C
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                   hypothetical protein AT4g01860 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 16 Feb-2001 #sequence_revision 16 Feb-2001 #text_change 16 Feb-2001
C;Accession: H85023
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488
A;Accession: H85023
A;Accession: H85023
A;Accession: H85023
A;Cacssrion: H8503
A;Cacssrion: H8503
A;Cacssrion: H8503
A;Cacssrion: H8503
A;Cacssr
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C; Species: S3807; Sosink, M.; Post, L.; Nomura, M.; Kestler, H.; Zengel, J.M.; Nucleic Acids Res. 13, 3891-3903, 1985
Nucleic Acids Res. 13, 3891-3903, 1985
A; Title: Nucleotide sequence of the alpha ribosomal protein operon of Escherichia coli.
A; Reference number: A23807; MUID: 85242076
A; Accession: A23807
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Pred. No. 1.8e+02;
2; Mismatches 0;
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Pred. No. 23;
1; Mismatches
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ilarity 83.3%;
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601 SLSVARL 607
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    1 MSIARL
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C; Superfamily: Escherichia coli ribosomal protein S13
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ó 0; Gaps Query Match
83.3%; Score 25; DB 2; Length 118;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels

1 SMSIARL 7 ||||| || 74 SMSIKRL 80 δy

qq

Search completed: May 8, 2002, 07:19:33 Job time: 101 sec

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Wed May 8 07:50:35 2002
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 8, 2002, 07:17:52; Search time 35.89 Seconds

(without alignments)
57.058 Million cell updates/sec

Ferfect score:

US-09-765-086-200

Perfect score:

1 KLAKLAKKLAKLAK 14

Scoring table:

BLOSUM62

1 Gapop 10.0, Gapext 0.5

Searched:

473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1: *p_archea:*
2: *p_bacteria:*
3: *p_fungl:*
4: *p_human:*
5: *p_namman:*
6: *p_mammal:*
7: *p_mammal:*
8: *p_organelle:*
9: *p_hage:*
10: *p_plant:*
11: *p_ordent:*
12: *p_virus:*
13: *p_virus:*
14: *p_unclassified:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_17:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O99xt3 streptococc	Q9v6r9 drosophila	09c7v6 arabidopsis	Q9jqq9 neisseria m	Q9x1h8 thermotoga	Q20191 caenorhabdi	P95826 streptococc	Q54839 streptococc	055246 streptococc	Q55278 streptococc	Q9pmr1 campylobact	Q55279 streptococc	033631 streptococc	Q55098 streptococc	Q54840 streptococc	Q55312 streptococc	Q00720 group g str	Q914n1 streptococc	09k5d4 campylobact
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Q03785 saccharomyc Q09958 caenorhabdi Q997u0 schizosacch Q9az19 bacteriopha	Q99ce7 aeropyrum p Q9ycp7 aeropyrum p Q48758 listeria mo Q93548 caenorhabdi Q9k614 bacillus ha Q9jsp0 neisseria m	Q58728 methanococc Q20873 caenorhabdi Q99733 staphylococ O14236 schizosacch Q9vxs2 drosophila Q9uy62 pyrococcus	Q9Uiq4 caenorhabdi Q9dwhB rat cytomeg Q9n4h7 caenorhabdi Q9xms2 tetrahymena O770G5 plasamodium Q9tv3Q olasmodium	067003 aquifex aeo 014222 homo sapien 099xw9 streptococc 09ulb6 leishmania
461 3 Q03785 462 5 Q09958 1184 3 Q9Y7U0 92 9 Q9A219	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	393 1 Q58728 412 5 Q20873 457 2 Q99R33 537 3 Q14236 684 5 Q9VXS2 758 1 Q9UY62	2 2 2 2 3	218 2 067003 227 4 014222 249 2 099XW9 295 5 09U1B6
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ALIGNMENTS

99XT3; PRELIMINARY; P 99XT3; PRELIMINARY; P 19XUN-2001 (TEMBLEE1. 17, Las 11-UN-2001 (TEMBLEE1. 17, Las 11-UN-2001) 12-UN-2001 (TEMBLEE1. 17, Las 11-UN-2001) 12-UN-2001 (TEMBLEEN. 17, Las 11-UN-2001) 13-UN-2001 13-UN-20	805 AA.	7	ce update) tion update)	.3.1.54).		ium group: Streptococcaceae	The state of the s					Savic D.J., Savic G., Lyon	enton S., Lai H.S., Lin S.F	Zhu H., Song L., White J.,	hiin K.;	563(2001).		ferase; Complete proteome.	3C41F1686D761B6E CRC64;	na 2. Ionath 805.	02; Tagala 0.	Z TINGETS		
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Query Match
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Matches 12; Conservative
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RAMAN-EMERILET;

RAMAN-
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0
                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43265 MW; 01409135653619F0 CRC64;
01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-WAY-2000 (TrEMBLrel. 13, Last annotation update) CG13333 PROFEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09C7V6 PRELIMINARY; PRT; 476 AA. 09C7V6; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) BZIP TRANSCRIPTION FACTOR, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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EMBL; AE003818; AAF58353.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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339 KLAELAKRLSTLA 351
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=7227;
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MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
Minte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Minte O., Alonso J., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Munter J. Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Munter J.L., Goldsmith A.D., Haass B., Hansen N.F., Hughes B., Hulzar L.,
Munter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Minter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Millischer J., Miranda M., Niguren W., Nierman W.C., Osborne B.I.,
Manitscher J., Miranda M., Niguren M., Nierman W.C., Osborne B.I.,
Manitscher J., Miranda M., Niguyen M., Nigoroy T., Rowley B.I.,
Manitscher J., Miranda M., Niguyen M., Nigoroy T., Rowley B.I.,
Manitscher J., Wan Man P.K., Rizzo M., Rooney T., Rowley B.I.,
Man G., Peterson J., Pam P.K., Rizzo M., Rooney T., Rowley B.I.,
Mu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
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01-OCT-2000 (TREMBLrel. 15, Last sequence update)
01-OCT-2000 (TREMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN NMA1321 (BASEPLATE ASSEMBLY PROTEIN V, PUTATIVE).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
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STRAIN-22491, SERGCROUP A / SERCOTYPE 4A;

STRAIN-22491, SERGCROUP A / SERCOTYPE 4A;

MEDLINE-2022556; PubMed-10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Bayles R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

Jagels K., Leather S., Moule S., Mingall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehed S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria

menigitidis 22491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 408:816-820(2000).
EMBL; AC066689; AAG51716.1; -.
SEQUENCE 476 AA; 55488 WW; D11027732F9C277C CRC64;
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57.1%; Pred. No. 2e+02;
ive 1; Mismatches
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Neisseria meningitidis (serogroup B).
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MEDLINE=20175755; PubMed=10710307;
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SEQUENCE

Matches

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Brandt E.R., Good M.F.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U66005; AAB40642.1;
                                                                                                                                                                                                                                                                                  Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: 269791; CAA93663.1; ...
EMBL; 269793; CAA93663.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 648 AA; 73405 MW; 1661914F3CEAC71E CRC64;
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208 AA; 22565 MW; 79972A987324729B CRC64;
                                                            Created)
Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 3.8e+02;
1; Mismatches 2;
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Pfam; PF00746; Gram_pos_anchor; 1.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1
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                           648 AA.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003502; ShKT.
InterPro; IPR0030130; Zn_MTpeptdse.
Pfam; PF01400; Astacin; 1.
SMART; SM00254; ShKT; 1.
SMART; SM00235; ZnMC; 1.
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                           PRT;
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EMBL; Z69791; CAA93676.1; JOINED.
HSSP; P28825; 11AF.
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73.38;
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                                         Q20191; Q21661;
01-NOV-1996 (TrEMBLrel. 01,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity 73.3
Matches 11; Conservative
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                           PRELIMINARY;
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                                                                                                                                                      Caenorhabditis elegans.
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Streptococcus pyogenes.
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                   F39D8.4 PROTEIN.
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NON_TER 1
NON_TER 208
SEQUENCE 208
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                     Q20191 F
Q20191; Q2166
01-NOV-1996 (
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P95826;
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Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Felstchmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Oln H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58";
Science 287:1809-1815(2000)
EMBL, AL162755; CAB84572.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEDGINE FOR W.H.

STRAIN-MSBB / DSM 3109;

MEDLINE-99287316; PubMed=10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heldelberg J., Sutton G.G., Flastomman R.D., Elsen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).

FNBL, AR001797; AAD36535.1; -.
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69.2%; Pred. No. 1.1e+02;
ive 2; Mismatches 2; Indels
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222 AA; 23251 MW; EOAFE240175C90DF CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
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PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
Complete proteome.
SEQUENCE 426 AA; 48981 MW; 9DEAFCBF27)
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InterPro; IPR002819; HD.
InterPro; IPR003607; HDc.
Pfam; PF01966; HD; 1.
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3 LSKLAKKTAQTAK 15
                                                                                                                                                                                                                                                                                                                                                                                                    2 LAKLAKKLAKLAK 14
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260 KVAELAKKIAK 270
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Best Local Similarity
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                                                                                                                                                                                                                             NMB1111; -.
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                                                                                                                                                                                                                                                 Hypothetical
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09х1нв; 09х1н8

RESULT 09X1H8

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Gaps

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Indels

Length 648;

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Length 208;
Score 39; DB 2;
Pred. No. 1.5e+02;
62.9%;
75.0%;
 Query Match
Best Local Similarity
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Matches

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STRAIN=C36;
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NON_TER
SEQUENCE
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SIGNAL
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055278;
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Q55278
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Q9PMR1
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J. Clin. Microbiol. 33:356-363(1995).
EMBL. X60098; CAA42694.1; -
EMBL. X60098; CAA42694.1; -
InterPro; IPR001899; Grampos_anchor.
InterPro; IPR001345; M_repeat.
Pfam; PF00746; Gram_pos_anchor; 1.
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   Gaps
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Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
Streptococcus.
NCBL_TaxID=1306;
                                                                                                                                                           Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Pred. No. 3e+02;
2; Mismatches 1; Indels
  Indels
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Last annotation update)
                                                                                                                   Last sequence update)
Last annotation update)
 1;
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Pfam; PF02370; M; 8.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                       436 AA
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 Mismatches
                                                                                                                                                                                                                                                        streptococci.";
Mol. Gen. Genet. 237:287-300(1993).
EMBL, x58179; CAA41168.1; -.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003345; M_repeat.
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MEDLINE=93204905; PubMed=8455563;
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G55246;
01-NOV-1996 (TrEMBLrel. 01, C:
01-NOV-1996 (TrEMBLrel. 01, L:
01-JUN-2001 (TrEMBLrel. 17, L:
M PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                     62.9%;
75.0%;
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01-NOV-1996 (TrEMBLEEL 01,
01-JUN-2001 (TrEMBLEEL 17,
M PROTEIN TYPE 52.
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Best Local Similarity 75.0
مارح 9; Conservative
 Conservative
                                                                                      PRELIMINARY;
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116 KLAKQAEELAKL 127
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                   1 KLAKLAKKLAKL 12
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                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                             Streptococcus.
NCBI_TaxID=1314;
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6
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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MEDLINE-94291620; PubMed-8020466;
MEDLINE-94291620; PubMed-8020466;
MEDLINE-94291620; PubMed-8020466;

"Streptokinase activates plasminogen bound to human group C and (streptococci through M-11ke proteins.";

EMEL, J. Blochem. 222.267-276(1994).

EMBL; 322677; CAA83588.1; -.
HSSP; P03069; 1GCL.

InterPro; IPR001899; Gram_pos_anchor.

InterPro; IPR001899; M_repeat.
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                                                                                                                                                  62.9%; Score 39; DB 2; Length 441; 75.0%; pred. No. 3.1e+02; Live 2; Mismatches 1; Indels
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Pfam; PF02370; M; 7.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM-POS_ANCHORING; UNKNOWN_1.
Actin-binding; Transmembrane.
SEQUENCE 441 AA; 49868 MW; 33DF991E365D9455 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MLC36 PRECURSOR (FRAGMENT).
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02370; M; 9.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                         454 AA.
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01-OCT-2000 (TrEMBLrel. 15, C)
01-OCT-2000 (TrEMBLrel. 15, Le
01-JUN-2001 (TrEMBLrel. 17, Le
PUTATIVE FUMARATE LYASE.
CJ1394.
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Matches 9; Conservative
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Matches 9; Conservative
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>454
454
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349 KLAKQAEELAKL 360
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389 KLAKQAEELAKL 400
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30 >4
454 4
454 AA;
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NCBI_TaxID=1306;
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407 KLAKQAEELAKL 418

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Streptococcus sp.
Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
NCBI_TaxID=1306;
                                                                                                                                                                                                                                                                                                        Streptococcus equisimilis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geyer A., Schmidt K.H.; "Genetic organisation of the M protein region in human isolates of group C and G streptococci: two types of multigene regulator-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.9%; Score 39; DB 2; Length 475
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 2; Mismatches 1; Indels
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STRAIN-GROUP C, C74A (ATCC 1238);
Podbielski A., Melzer B.;
Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; X60097; CAA42693.1; -.
HSSP; P03069; 1GCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES-S.dysgalactiae subsp. equisimilis; STRAIN-25287;
MEDLINE-20123454; PubMed-10660058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-S equisimilis; STRAIN=25287;
Geyer A., Schmidt K.H.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                           03361;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
M-LIKE PROTEIN.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
M PROTEIN.
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PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                             475 AA.
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Mol. Gen. Genet. 262:965-974(2000).
EMBL; X93464; CAA63750.1;
EMBL; Y18363; CAB70608.1;
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor;
Pfam; PF00746; Gram_pos_anchor;
Pfam; PF00370; M; No.
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InterPro; IPR003345; M_repeat.
Pfam; PF00746; Gram_pos_anchor; 1.
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| 383 KLAKQAEELAKL 394
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                                                                                                                                                                                                                                                                                                                                                             Streptococcus.
NCBI_TaxID=119602;
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033631
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                                                                                                                               SEQUENCE FROM N.A.

STRAIN-WITC 11168

STRAIN-WITC 11168

MEDLINE-20150912; PubMed-10688204;

MEDLINE-20150912; PubMed-10688204;

MEDLINE-20150912; PubMed-10688204;

MEDLINE-20150912; PubMed-10688204;

MEDLINE-20150912; PubMed-1068204;

MEDLINE-20150912; PubMed-1068204;

Magals K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Magals K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Mitchead S., Barrell B.G.;

Mitchead S., Barrell B.G.;
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Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
NCBI_TaxID=197;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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"Streptokinase activates plasminogen bound to human group C and G
"Streptokinase activates plasminogen bound to human group C and G
Eureptococci through M-like proteins.";
EMBL, 232678; CAA83589.1; -.
EMBL, 232678; CAA83589.1; -.
EnterPro: IRRO01899; Gram_pos_anchor.
InterPro: IRRO01345; M_repeat.
PROSITE; PSO0343; GRAM_POS_ANCHORING; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.9%; Score 39; DB 2; Length 455; 64.3%; Pred. No. 3.2e+02; tive 2; Mismatches 3; Indels
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8DE0886B2F45FFC8 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MLG72 PRECURSOR.
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MEDLINE-94291620; Pubmed-8020466;
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472 AA; 53968 MW;
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Best Local Similarity 64.3.
Best Local 9; Conservative
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131 ELKAIAKALAKLAK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
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STRAIN-SEROTYPE M55;
MEDLINE-95371690; PubMed=7643859;
MEDLINE-95371690; PubMed=7643859;
A BOYLE M.D.P., Weber-Heymemann J., Raeder R., Podbielski A.;
Characterization of a gene coding for a type IIo bacterial IgG-
T binding protein..;
Mol. Immunol. 32:669-678(1995).
R EMBL; X72090; CAA50980.1; -.
IR PEMBL; X72090; CAA50980.1; -.
R PRINTS; PRO0015; Gram_pos_anchor.
R Pfam; PF00746; Gram_pos_anchor.
R PRINTS; PR0015; GPOSANCHOR.
R PRINTS; RS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
W TRANSMEMBLY ARD AA, 61736 MW; 32894BFF9805181B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes.

Bacillus/Clostridium group; Streptococcaceae; Streptococcus.

Streptococcus.

NCBI_TaxID-1314;
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                                                                                                                                                                                                                                                                          Query Match 62.9%; Score 39; DB 2; Length 532; Best Local Similarity 75.0%; Pred. No. 3.7e+02; Matches 9; Conservative 2; Mismatches 1; Indels
Pfam; PF02370; M; B.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
Transmembrane.
SEQUENCE 532 Aa; 60362 MW; 4Ala78B9D1122787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   054840 PRELIMINARY;
054840 01-NOV-1996 (TrEMBLrel. 01, Cr
01-NOV-1996 (TrEMBLrel. 01, La
01-JUN-2001 (TrEMBLrel. 17, La
M PROTEIN.
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AC 054840;
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Search completed: May 8, 2002, 07:20:14 Job time: 142 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2002, 07:17:52; Search time 12.86 Seconds May Run on:

(without alignments) 39.915 Million cell updates/sec

US-09-765-086-200 62

1 KLAKLAKKLAKLAK 14 Perfect score: Sequence:

BLOSUM62

Scoring table:

100059 seqs, 36664827 residues Gapop 10.0 , Gapext 0.5 Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		esche		P43718 haemophilus			_	Q13416 homo sapien	_	Q05783 drosophila	_			P44857 haemophilus		-			P06893 xenopus lae	_	Q9zju8 helicobacte	P93253 mesembryant	Q01781 petroselinu		P40368 saccharomyc	_	P46307 chlamydomon		Q00383 epifagus vi		Q9uxg7 sulfolobus	P75442 mycoplasma	P50470 streptococc
SUMMARIES	ID	В	YCAL_ECOLI	M24_STRPY	ATPE_HAEIN	H1G_STRPU	YJ86_YEAST	Y811_METJA	ORC2_HUMAN	MST2_DROHY	HMGD_DROME	Y269_MYCGE	GSA_CAMJE	CORO_SCHPO	PLSB_HAEIN	NOT3_YEAST	SYV_ECOLI	RPC1_BPP22	FAB3_CAEEL	H1B_XENLA	RPOD_PYRHO	TRPC_HELPJ	SAHH_MESCR	SAHH_PETCR	SAHH_TOBAC	NU82_YEAST	SPOT_MYCGE	RR3_CHLEU	MANB_CAEEL	YCF1_EPIVI	POLN_RRVN	KTH1_SULSO	Y240_MYCPN	SPH_STRPY
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de	Query Match	69	62.9	62.9	61.3		61.3				59.7	59.7	59.7	59.7	59.7	59.7	59.7	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	56.5	56.5	56.5
	Score	43	39	39	38	38	38	38	38	38	37	37	37	37	37	, 37		36	36	36	36	36	36	36	36	36	36	36	36	36	36	32	32	32
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Pfam; PF01388; ARID; 1.
Pfam; PF02373; JmJC; 1.
Pfam; PF02375; JmJN; 1.
Pfam; PF00628; PHD; 3.
SMART; SM00501; BRIGHT; 1.

InterPro; IPR001606; ARID. InterPro; IPR003347; JmjC. InterPro; IPR003349; JmjN. InterPro; IPR001965; PHD.

P13050 streptococc P30141 streptococc P49054 streptococc P16947 streptococc P50468 streptococc 004658 arabidopsis P12782 triticum ae P36100 saccharomyc P08089 streptococc P5007 catharanthu P37556 bacillus su
ARP4 STRPY MRP4_STRPY M49_STRPY M21_STRPY Y412_ARATH PGKH, WHEAT T2EA_YEAST M6_STRPY SAHH_CATRO YABN_BACSU
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE RETINOBLASTOMA PROTEIN.
-1- SUBCELLIDIAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: TO THE C-TERMINAL DOMAIN OF THE XE169 PROTEIN AND THE JUMONJI PROTEIN A
                                                                                                                                                                                                                                                                                                                                                                         SEMUNICE OF 1102-1569 FROM N.A.

SEMUNICE-91312450; PubMed=1857421;
MEDLINE-91312450; PubMed=1857421;
Defeo-Jones D., Hubar H.E., Oliff A.;
Hanobik M.G., Hubar H.E., Oliff A.;
Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene product.";
retinoblastoma gene product.";
Nature 352:211-254(1991).
Nature 352:211-254(1991).
                                                                                                                                                                                                                                MEDLIND=94020841; PubMed=8414517;
Fattaey A.R., Helin K., Dembski M.S., Dyson N., Harlow E.,
Vuocolo G.A., Hanobik M.G., Haskell K.M., Oliff A., Defeo-Jones D.,
Jones R.E.;
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                     'Characterization of the retinoblastoma binding proteins RBP1 and
                                                 01-DEC-1992 (Rel. 24, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
02-0CT-02UG-2001 (Rel. 40, Last annotation update)
RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).
                PRT; 1722 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S66431; AAB28544.1; -.
                                                                                                                                                                                                                                                                                                                                                        Oncogene 8:3149-3156(1993).
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S16954; S16954.
MIM; 180202; -.
                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
MEDLINE-94020841;
                  RBB2_HUMAN
RBB2_HUMAN
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RESULT
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
Corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97426617; PubMed-9278503;
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95138007; PubMed-7836281;
Fricke J., Neuhard J., Kelln R.A., Pedersen S.;
"The cmk gene encoding cytidine monophosphate kinase is located in the rpsA operon and is required for normal replication rate in Escherichia coli.";
J. Bacteriol. 177:517-523(1995).
                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palma C.A., Allen E., Araujo R., Aparicio A.M., Botstein D., Cherry M., Chung E., Dietrich F., Duncan M., Federspiel N., Kalman S., Kim K., Komp C., Lashkari D., Lew H., Lin D., Namath A., Oefner P., Davis R.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                        DB 1; Length 1722;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gregor J., Davis N.W., Kirkpalitch m.n., vocated by Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
SMART; SM00545; JmjN; 1.
SMART; SM00249; PHD; 3.
Trans-acting factor; Nuclear protein.
CONFLICT 1563 1566 MISSING (IN REF. 2).
SEQUENCE 1722 AA; 195815 MW; 8CFF8A88AE69A652 CRC64;
                                                                                                               Indels
                                                                                                                                                                                                                         YCAL_ECOLI STANDARD; PRT; 254 AA. P43674; P75840; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) PUTATIVE METALLOPROTEASE YCAL (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METALLOPROTEASE). STRONG, TO E.COLI YGGG.
                                                                                      Score 43; DB 1
Pred. No. 40;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 150-254 FROM N.A.
                                                                                      69.4%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-183 FROM N.A.
                                                                                     Query Match 69.4
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                              1552 KLNKLAKKLAK 1562
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                                                                                                                                      1 KLAKLAKKLAK 11
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                                                                                                                                                                                                                                                                                                                Escherichia coli.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC (CATALYTIC) (POTENTIAL).
ERAGHIRDRIASGK -> DVRNTSVIVSPLVSKSLSSLRWS
SASPL (IN REF. 3).
ADDF70D17E9D93A0 CRC64;
between the Swiss Institute of Bioinformatics and the EMBL outstati
the Buropean Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as luga as its content is in no
modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
-:- SIMILARITY: TO OTHER W PROTEINS.
-:- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 62.9%; Score 39; DB 1; Length 254; Best Local Similarity 57.1%; Pred. No. 30; Matches 8; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC (CATALYTIC) (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01435; Peptidase_M48; 1.
Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-00T-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                539 AA.
                                                                                                                                                                                              EMBL; AE000193; AAC73995.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                           IPR001915; Peptidase_M48.
                                                                                                                                                                                                                        EMBL; D90728; BAA35644.1; -.
EMBL; D90729; BAA35653.1; -.
EMBL; U31523; AAA81515.1; ALT_INIT.
EMBL; X82933; CAA58106.1; -.
MEROPS; M48.006; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Vaughn / Serotype M24;
MEDLINE=88115166; PubMed=3276665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26740 MW;
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                                                                                                                                                                                                                                                                                                                                                                 EcoGene; EG13133; ycaL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M24_STRPY
ID M24_STRPY
AC P12379;
                                                                                                                                                                                                                                                                                                                                                                                                interPro;
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CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                   2 (1 ALTERATION).
3 (2 ALTERATIONS).
4 (1 ALTERATIONS).
5 (2 ALTERATIONS).
6 (INCOMPLETE).
7 X 35 AA TANDEM REPEATS, B-TYPE.
                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
5.3 X 35 AA TANDEM REPEATS, A-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whole-genome random sequencing and assembly of Haemophilus
                                                                                          PRINTS; PRO0015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Signal; Virulence; Cell wall; Transmembrane; Phagocytosis;
Duplication; Repeat; Antigen; Coiled coil.
SIGNAL 1 42 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 1; Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                     POTENTIAL.
M PROTEIN, SEROTYPE 24.
EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                           B03EDF3AC1E6E9C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 57;
2; Mismatches
             EMBL; M19031; AAA26874.1; -.
PIR; A28549; A28549; A28549; IPR001899; Gram_pos_anchor.
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                 Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF02370; M; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                         539 AA; 58804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.9
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 KLAKQAEELAKL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLAKLAKKLAKL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPC OR HI0478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                influenzae Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATPE_HAEIN
P43718;
                                                                                                                                                                  CHAIN
DOMAIN
TRANSMEM.
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                                                                                                                                                                                                           DOMAIN
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DOMAIN
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REPEAT
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REPEAT
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REPEAT
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE EPSILON CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDIINE-87172742; PubMed=3031476; MEDIINE-87172742; PubMed=3031476; Knowles J.A., Lai Z.-C., Childs G.J.; Knowles J.A., Lai Z.-C., and expression of the gene encoding the "Isolation, characterization, and expression of the gene encoding the late histone subtype H1-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purpuratus.";
Mol. Cell. Biol. 7:478-485(1987).

-i. FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.

-i. SUBCELLULAR LOCATION: NUCLEAR.

-i. SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                              142 AA; 15591 MW; E5BBDE1DA34A9039 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A26721; A26721.
HSSP: P02259; 1HST.
InterPro: IPR001386; Linker_histone.
InterPro; IPR003216; Linkerhist_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001469; ATP-synt_DE.
Pfam; PF00401; ATP-synt_DE; 1.
ProDom; PD000944; ATP-synt_DE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.3%;
72.7%;
                                                                                                                                                                                                                                                                                  EMBL; U32730; AAC22136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M16033; AAA30059.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HISTONE H1-GAMMA, LATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||:|:||:|
118 VAKLSKELAKL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus.
                                                                                                                                                                                                                                                                                                       HSSP; P00832; 1BSH.
TIGR; HI0478; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
SEQUENCE 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H1G_STRPU
P07796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                               DEDUCATE ROLA WIGH.

STRAIN-JAL-1 DSW 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=868087;

MEDLINE=96337999; PubMed=868087;

Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness B.F., Weilnstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hilley M., Kaine B.P., Borodorsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                           Science 273:1058-1073(1996).
-!- SIMILARITY: TO M.JANNASCHII MJ0077 AND SOME, TO E.COLI YIEM.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.3%; Score 38; DB 1; Length 439; 69.2%; Pred. No. 67;
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: 2F85F2B942C1CDFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-96099401; Pubmed=7502077;
Gavin K.A., Hidaka M., Stillman B.D.;
Conserved initiator proteins in eukaryotes.";
Science 270:1667-1671(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORC2_HUMAN STANDARD; PRT; 577 AA. 013416; 013204; STO NOV-1997 (Rel. 35, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) ORC2L OR ORC2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTON, CO. 178002035; VWFA.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67525; AAB98810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.3
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
REVISIONS TO 41-42.
Hidaka M., Stillman B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLAKLAKKLAKLA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein;
DOMAIN 273 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 439 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                 iannaschii.
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                                                                                                                                                                                 Gaps
                ProDom; PD000373; Linkerhist_N; 1.
SMART; SMO526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 217 AA; 22658 WW; C7251EED3413B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fundi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_FaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 32.0 KDA PROTEIN IN NNF1-STE24 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 279;
Pred. No. 45;
                                                                                                                                       Length 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Rose M., Koetter P., Entian K.D.,
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6610293B38B7F2B5, CRC64;
                                                                                                                                     DB 1;
36;
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ID Y811_METJA STANDARD; PRT; 439 AA.
AC QS8221.
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 00-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DF HYPOTHETICAL PROTEIN MJ0811.
                                                                                                                                                                                                                                                                                                                                                             279 AA.
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                     Score 38;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                             PRT;
Pfam; PF00538; linker_histone; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.3%;
61.5%;
                                                                                                                                     61.3%;
71.4%;
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                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                            1 KLAKLAKKLAKLAK 14
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261 KMIRIAKKLAKPA 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
193
239
279 AA;
                                                                                                                                     Ouery Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             YJ86_YEAST
P47153;
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                                                                                                                                                                                                                                                                                                                       RESULT 6
YJ86_YEAST
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Matches
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Gaps

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Indels

us-09-765-086-200.rsp

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melanogaster
                                                      REPEATS.
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Best Local
                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                   A Takahara K., Bong M., Brevard R., Eddy R.L., Haley L.L., Sait S.J.,
A Takahara K., Bong M., Brevard R., Eddy R.L., Haley L.L., Sait S.J.,
Shows T.B., Hoffman G.G., Greenspan D.S.;
Mouse and human homologues of the yeast origin of replication
T ecognition complex subunit ORC2 and chromosomal localization of the
cognate human gene ORC2L.";
Genomics 31:119-122(1996).

-!- FUNCTION: COMPONENT OF THE ORIGIN RECCGNITION COMPLEX (ORC) THAT
BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL
REPLICATION AND MATING TYPE TRANSCRIPPIONAL SILENCING. BINDS TO
THE ARE CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN
ATP-DEPENDENT MANNER.
-!- SUBGRILLUAR LOCATION: NUCLEAR.

-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: BELONGS TO THE ORC2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pteryyota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila, (CBL_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95045538; PubMed-7957199; Neesen J., Padmanabhan S., Buenemann H.; Tandemly arranged repeats of a novel highly charged 16-amino-acid motif representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmst101 form extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-helical rods within the extremely elongated spermatozoa of Dosophila hydei.";
Eur. J. Biochem. 225:1089-1095(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.3%; Score 38; DB 1; Length 577; llarity 72.7%; Pred. No. 85; Conservative 2; Mismatches 1; Indels
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DF3F9C2CF147DA5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    I -> V (IN REF. 3).
T -> L (IN REF. 3).
I -> M (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
AXONEME-ASSOCIATED PROTEIN MST101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                     DNA replication; Nuclear protein. CONFLICT 131 131 1->
                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 AA; 65971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MST101(2).
Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                               EMBL; U40268; AAC50326.2; -. EMBL; U27459; AAB33970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       131
236
392
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Best Local Similarity
'`^a 8; Conserv?
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105 KMAKLASELAK 115
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                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MST2_DROHY
Q08696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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SPERMATIDS.
--- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
--- POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
--- STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CANTON-S;
MEDLINE=94(21387; PubMed=8414994;
MEDLINE=94(21387; PubMed=84144994;
Mer S.S., Churchill M.E.A., Searles M.A., Travers A.A.;
"dHMG-Z, a second HMG-1-related protein in Drosophila melanogaster.";
Nucleic Acids Res. 21:4369-4371(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 10.2. Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HMGD_DROME STANDARD; PRT; 112 AA. 005783; Q9W2D3; 01-FEB-1995 (Rel. 31, Created) 20-FEB-1995 (Rel. 31, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIGH MOBILITY GROUP PROTEIN D (HMG-D). HMGD OR CG17950.
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MEDLINE=92236564; PubMed=1373803;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X73481; CAA51876.1; -. PIR; S34154; S34154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
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9

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Gaps

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3; Indels

2; Mismatches

Ouery Match 59.7%; Best Local Similarity 64.3%; Matches 9; Conservative

1 KLAKLAKKLAKLAK 14

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Score 37; DB 1; Length 112; Pred. No. 29;

protein; Chromosomal protein; DNA-binding; 3D-structure.

PDB; 1HMA; 31-7UL-94.
FlyBase; FBGN0004362; HmgD.
InterPro; IPR000910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
SMARY; SM00398; HMG; 1.

EMBL; M77023; AAA28609.1; -. EMBL; AE003455; AAF46759.1; PIR; A44382. PIR; S32724; S32724.

ASP/GLU-RICH (ACIDIC). 3F537CCFD62FEC9F CRC64;

12416 MW;

112 AA;

SEQUENCE DNA_BIND DOMAIN

112

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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkva D., Botchan M.R., Bouck J., Brokstein P., Botshakov S., Burtis K.C., Busemn D.A., Butler H., Cadieu E., Center A., Chandra I., Reberry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., P. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rolser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., R. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harrey D., Hainan T.J., Hennandez J.R., Houck J., R. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A., Liu X., Mattei B., McIntosh T.C., Morris J., Moshrefi A., Murkutei B., McIntosh T.C., Morris J., Moshrefi A., Murkutei B., McIntosh T.C., Morris J., Moshrefi A., Mullshina N.V., Mobarry C., Morris J., Puri V., Reese M.G., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden Kalmon G.S., Pan S., Pollard J., Puri V., Raps S., Pollard J., Puri V., Wang S., Pao Q., Sheng E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Zhong G., Zhao Q., Zhao Gibbs R.A., Weinstock G.M., Weissenbach J., Mang C.-P., Wang S., Pollard J.C., Rapenger E.W., Rubing W., Zhong Y., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu S., Zhu S., Zhu K., The Genome sequence of Drosophila melanogaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Travers A.A.;
"HMG-D is an architecture-specific protein that preferentially binds
to DNA containing the dipucleotide TG.";
EMBO J. 14:1264-1275(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "HMG-D, the Drosophila melanogaster homologue of HMG 1 protein, is associated with early embryonic chromatin in the absence of histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE-95237208; PubMed=7720717;
Churchill M.B.A., Jones D.N.M., Glaser T., Hefner H., Searles M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 2-74.

STRUCTURE BY NMR OF 2-74.

MEDLINE-95006330; PubMed-7922039;
Jones D.N.M., Searles M.A., Shaw G.L., Churchill M.E.A., Ner S.S.,

Keeler J., Travers A.A., Neuhaus D.;

Keeler J., Travers A.A., Neuhaus D.;

"The solution structure and dynamics of the DNA-binding domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE=94222028; PubMed=8168480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 13:1817-1822(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ner S.S., Travers "HMG-D, the Drosop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEGUENCE FROM N.A.
SEGUENCE FROM N.A.
SETAINA-ATCC 3350 / G-37;
MEDLINE-96026346; PubMed-756993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Flictchman J.L., Weidmann J.F., Sandak D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 35530 / G-37;
MEDILTE-94075230; Pubmed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 340 AA; 39662 MW; 3921FE1F81501CC4 CRC64;
                                                                                                                                                                                                                                            Y269_MYCGE STANDARD; PRT; 340 AA. 049407; 049328; Created) 01-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 175:7918-7930(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U39706; AAC71491.1; -.
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Mycoplasma genitalium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2097;
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EMBL; X71138; CAA50468.1; -.

601 AA.

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PRT;
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InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 3.
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57.1%;
                                                                               CORONIN-LIKE PROTEIN CRN1.
CRN1 OR SPAC23C4.02.
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 STANDARD;
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=727;
                                15-JUL-1998
15-JUL-1998
                                                                 20-AUG-2001
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P44857;
 CORO_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- CATALYTIC ACTIVITY: (S)-4-AMINO-5-OXOPENTANOATE = 5-
AMINOLEGULIANE.
-1- COFACTOR: PYRIDOXAL
-1- PATHWAY: PORPHYRIN BIOSYNTHESIS BY THE C5 PATHWAY; SECOND STEP.
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: CYTOPLESHIC (POTENTIAL).
-1- SUBCELLULAR LOCATION: CYTOPLESHIC (POTENTIAL).
-1- SIMILARITY: BELONGS TO CLASS-111 OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                              Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRIDOXAL PHOSPHATE (BY SIMILARITY). 7811526A5AEDA57D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                          20-Aug-2001 (Rel. 40, Created)
20-Aug-2001 (Rel. 40, Last sequence update)
20-Aug-2001 (Rel. 40, Last annotation update)
GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOWUTASE (EC 5.4.3.8) (GSA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 72.7%; Score 37; DB 1; Length 424; Similarity 72.7%; Pred. No. 92; 8; Conservative 1; Mismatches 2; Indels
Score 37; DB 1; Length 340;
Pred. No. 76;
                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphyrin biosynthesis; Isomerase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL139076; CAB73118.1; -.
InterPro; IPR000954; Aminotran_3.
Pfam; PF00202; aminotran_3; 1.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; FALSE_NEG
                                                                                                                                                                                  424 AA.
                                3; Mismatches
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 AA; 46092 MW;
59.7%;
58.3%;
                                Conservative
                                                                                                                                                                                  STANDARD;
                                                                                  ||| ||:|::|
271 AKLTKKIAEITK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMINOTRANSFERASES
                                                               3 AKLAKKLAKLAK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 KLGKLAKKLTQ 332
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             Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-NCTC 11168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                HEML OR CJ0853
                                                                                                                                                                               GSA_CAMJE
Q9PP70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
 Query Match
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CORO_SCHPO
                                                                                                                                                               GSA_CAMJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=972;
Harris D., Squares R., Barrell B.G., Rajandream M.A., Wood V.;
Harris D., Squares R., Darrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/Genbank/DDBJ databases.
-1. SUBGNIT: BINDS TO F-ACTIN (BY SIMILARITY).
-1. SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
-1. SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
02-NGC-2001 (Rel. 40, Last annotation update)
GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.15) (GPAT).
PLSB OR H10748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL).
231096AE76CADE4D CRC64;
                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIMIS; PROGOZO, GPROTEINBRPT.
SMART; SW00320; GPROTEINBRPT.
SMART; SW00320; WD40; 3.
PROSITE; PS00062; WD_REPEATS_1; 1.
PROSITE; PS50294; WD_REPEATS_2; 3.
Actin binding; Repeat; WD_repeat; Coiled coil.
REPEAT 132 172 WD 2.
REPEAT 132 172 WD 2.
REPEAT 220 260 WD 4.
REPEAT 226 306 WD 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Pred. No. 1.2e+02;
(Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            810 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
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Riles L., Rowley N., Skelton J., Smith V.,

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Search completed: May
Job time: 161 sec
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          RRARRERAR RARRERAR RRARRERAR RRARRERAR RRARRERAR RRARRERAR RRARRERAR RRARRER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: ACYL-COA + GLYCEROL 3-PHOSPHATE = COA +
1-ACYL-GLYCEROL 3-PHOSPHATE.
-!- PATHWAY: DE NOVO PHOSPHOLIPID BIOSYNTHESIS; FIRST STEP. MAY ALSO
PATHWAY: THE REGULATION OF MEMBRANE BIOGENESIS.
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GPAT / DAPAT FAMILY.
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shriley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geognagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86312926; PubMed=3018676;
Ferguson J., Ho J.-Y., Peterson T.A., Reed S.I.;
Nucleotide sequence of the yeast cell division cycle start genes
CDC28, CDC36, CDC37, and CDC39, and a structural analysis of the
predicted products.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.7%; Score 37; DB 1; Length 810 63.6%; Pred. No. 1.68+02; uismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810 AA; 92774 MW; DB8564BC3E2C370D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 14:6681-6697(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-FEB-1995 (Rel. 31, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32758; AAC22406.1; -. TIGR; HI0748; -.
                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 63.6 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 KIAQKLARVAK 195
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                                                                                                                                                                                                                                                                          influenzae Rd.
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P06102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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NOT3_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
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                                                                                                                                                                                                                                                   Genes Dev. 8:525-537(1994).

-1- FUNCTION: NEGATIVELY REGULATES THE BASAL AND ACTIVATED TRANSCRIPTION OF MANY GENES. PREFERBYTALLY AFFECTS TC-TYPE TATA ELEMENT-DEPENDENT TRANSCRIPTION. COULD DIRECTLY OR INDIRECTLY INHIBITS COMPONENT(8) OF THE GENERAL TRANSCRIPTION MACHINERY.
-1- SUBGNIT: FORMS A COMPLEX THAT COMPRISE NOT1, NOT2, NOT3, NOT4 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CAUTION; WAS ORIGINALLY (REF.1) THOUGHT TO BE CDC29 (WHICH IS IN
                                                                                                                                            Collart M.A., Struhl K.; NOT3, and NOT4 encode a global-negative regulator of transcription that differentially affects TATA-element utilization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on regulation; Repressor; Coiled coil.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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Pred. No. 1 7e+02;
.; Mismatches 3; Indels
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I -> N (IN REF. 1).
Y -> C (IN REF. 1).
KQLKQGKISV -> ETIETGKN (I)
69B76694FCC6846F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: TO YEAST NOT5.
                                                                                                                  MEDLINE-95011559; PubMed=7926748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
Μ
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Best Local Similarity 69.2
Matches 9; Conservative
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725
836
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803
106
725
827
836 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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8, 2002, 07:20:33

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Мау

8, 2002, 07:17:52; Search time 22.68 Seconds (without alignments) 47.021 Million cell updates/sec

US-09-765-086-200 62

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 KLAKLAKKLAKLAK 14 Perfect score: Scoring table: Sequence:

219241 seqs, 76174552 residues Searched: 219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	retinoblastoma bin	hypothetical prote	baseplate assembly	conserved hypothet	hypothetical prote	probable heat shoc	cmk protein precur	M protein precurso	plasminogen-bindin	probable fumarate	plasminogen-bindin	M protein - Strept	M24 protein precur	Fc gamma (IgG) rec	H+-transporting AT	histone H1-gamma,	probable membrane	hypothetical prote	probable membrane	hypothetical prote	coiled coil protei	sperm tail-specifi	high mobility grou	probable gastrin p	hypothetical prote	~	surface protein an	probable rotamase	· GTP-binding protei
SUMMARIES	ID	178879	B96667	D81122	D72252	T23864	F85616	D64830	S30284	S43556	D81284	S43554	S54871	A28549	JC1419	C64071	A26721	S57139	C64401	S54543	T15543	T41515	S51364	A44382	B72593	T21215	C84114	G64229	A81794	C64466
	DB	-																	7											7
	& Query Match Length	1722	476	222	426	648	262	262	436	454	455	472	532	539	587	142	217	279	439	461	462	1184	1390	112	127	246	282	340		393
•	Query Match	69.4	65.3	64.5	64.5	63.7	62.9	62.9	62.9	62.9	62.9	62.8	62.8	62.9	62.9	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	59.7	59.7	59.7	59.7	59.7	59.7	59.7
	Score	43	40.5	40	40	39.5	39	39	39	39	39	39	39	39	39	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37
	Result No.		7	3	4	S	9		80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote glutamate-1-semial	hypothetical gtp-b coronin-like prote	hypothetical prote hypothetical prote	glycerol-3-phospha cell division cont	valinetRNA ligas	valine tRNA synthe requlatory protein	trans-regulatory p	histone H1B - Afri	translation elonga	adenosylhomocystei
T16480 E81358	T39037 T38258	T27465 H75013	D64090 S49940	SYECVT	E86124 Z1BPC2	H70371	151447	154251	T15035
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412	537 601	634 758	810 836	951	951 92	218	220	227	227
59.7	59.7 59.7	59.7	59.7	59.7	59.7 58.1	58.1	58.1	58.1	58.1
37	37	37	37	37	37	36	36	36	36
30 31	32 33	34 35	36	38	39 40	41	43	44	4.5

ALIGNMENTS

C,Accession: I78879; S16954
R;Fattaey, A.R.; Helin, K.; Dembski, M.S.; Dyson, N.; Harlow, E.; Vuocolo, G.A.; Hano Oncogene B, 3149-3156, 1993
A;Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
A;Reference number: I58383; MUID:94020841
A;Accession: I78879 A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1722 <RNA
A; Residues: 1-1722 <RNA
A; Cross-references: GB:S66431; NID:9435777; PIDN:AAB28544.1; PID:9435778
B; Defeo-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M Nature: 352, 251-254, 1991
Nature: Cloning of conna for cellular proteins that bind to the retinoblastoma gene
A; Reference number: S16953; MUID:91312450 C;Species: Homo sapiens (man) C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000 A; Status: not compared with conceptual translation retinoblastoma binding protein 2 - human A; Accession: S16954

A;Map position: 3q21-3qter C;Superfamily: human retinoblastoma binding protein 2 A;Gene: GDB:RBP2 A;Cross-references: GDB:119548; OMIM:180280 A, Molecule type: mRNA A, Residues: 1102-1562, 'KKK' <DEF> C;Genetics:

ö Query Match
Best Local Similarity 90.9%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 1; Indels

ö

Gaps

|| |||||||| | 1552 KLNKLAKKLAK 1562 1 KLAKLAKKLAK 11 g ŏ

RESULT

hypothetical protein F15H21.20 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C; Accession: B9667
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, W.K.; Connon, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hundrer, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Gaps

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Indels

Length 426;

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C; Species: Escherichia coli (C; Date: Becherichia coli (B; Derna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A; Fatile: Genome sequence of enterohemorrhagic Escherichia coli (Di57:H7. A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: F85516
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-262 <STO>
                                                                                 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316
A;Recession: D72252
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <ARNN
A;Residues: 1-426 <ARNN
A;Reperimental source: GB:AE001797; GB:AE000512; NID:g4982017; PIDN:AAD36535.1; PID:g498
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE005174; NID:g12514075; PIDN:AAG55394.1; GSPDB:GN00145; UWGP: A;Cross-references: strain 0157:H7, substrain EDL933 C;Genetics: A;Gene: yçaL
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable heat shock protein ycaL [imported] - Escherichia coli (strain 0157:H7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: X
A;Introns: 22/2; 112/3; 160/1; 250/1; 334/1; 424/3; 463/1; 485/3; 528/2; 593/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:269793; PIDN:CAA93676.1; GSPDB:GN00028; CESP:F39D8.4 A;Experimental source: clone R03A10 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F39D8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Late: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T23864
R;Hembry, C.
submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: 219809
A;Accession: T23864
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7
66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.7%;
73.3%;
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376 KLAKLGOKLGKTLAK 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|:||||:||
260 KVAELAKKIAK 270
                                                              Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLAKLAKKLAK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-648 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP: F39D8.4
                                                                                                                                                                                                                                                                                                                                                                      A; Gene: TM1467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daseplate assembly protein V, probable NMB1111 [imported] - Neisseria meningitidis (stra Cispecies: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: DB1122; A81901
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; It, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Fizza, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Molecule type: DNA
A.Residues: 1-22 < TETP.
A.Residues: 1-22 < TETP.
A.Residues: 1-22 < TETP.
A.Experimental source: serogroup B, strain MC58
R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Rlee, S.R.; Morel
R. Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A.Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84572.1; PID:g737999
A,Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Accession: D72252
R; Nelsón, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ve
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
A; Accession: B9667
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-476 <STO>
A; Cross-references: GB:AE005173; NID:g10645403; PIDN:AAG21521.1; GSPDB:GN00141
A; Genetics:
A; Genetics:
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Reference number: A81000; MUID:20175755 A; Recession: D81122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 476;
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37;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 KLSKLEKKLAEEGTEKLKLAK 413
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69.2%;
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LSKLAKKTAQTAK 15
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: 1-222 <PAR>
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Gaps

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Indels

Length 648;

Gaps

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C;Accession: $45598; $43556
R;hen Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoebring, U.
Bur. J Biochem. 222, 267-276, 1994
A;Fitle: Streptokinase activates plasminogen bound to human group C and G streptococc
A;Reference number: $45598; MUID:94291620
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C;Accession: D81284
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba
Nature 403, 665-668, 2000
A;Tille: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A;Reference number: A81250; MUID:20150912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-455 <PAR>
A; Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73819.1; PID:g696
A; Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable fumarate lyase Cj1394 [imported] - Campylobacter jejuni (strain NCTC 11168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Streptococcus sp.
C;Date: 14-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA_A;Residues: 1-454 <BE2>A;Residues: BBL:Z32677; NID:g474767; PIDN:CAA83588.1; PID:g474768 C;Superfamily: M5 protein
A; Wolecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-216, N', 218-436 < POD2> A; Cross-references: EMBL:X58179; NID:947364; PIDN:CAA41168.1; PID:947365 C; Genetics: A Gene: emm C; Genetics: emm C; Superfamily: M5 protein C; Keywords: transmembrane protein C; Keywords: transmembrane protein F; 1-41.70main: signal sequence #status predicted <SIG> F; 42-436/Product: M protein #status predicted <MMT> F; 1-42/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasminogen-binding protein MLC36 - Streptococcus sp. (fragment)
                                                                                                                                                                                                                                                                                                                                                     Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 2; Pred. No. 99; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2
Pred. No. 96;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
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C,Superfamily: fumarate hydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.9%;
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                               Query Match 62.9%;
Best Local Similarity 75.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 KLAKQAEELAKL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLAKLAKKLAKL 12
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Best Local Similarity
Thes 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: D81284
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                                                                                                                                                                                                                                                                                                                                                                          cmk protein precursor - Escherichia coli
C;Species: Escherichia coli
C;Species: L2-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: D64830; 141019; 549998
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
A:; Rose, D.J.; Mau, B.; Shao, Y.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: D64830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Cross-references: GB:AE000193; GB:U00096; NID:91787134; PIDN:AAC73995.1; PID:91787138; A.Cross-references: Strain K12, substrain M01655
R.Fricke, J.; Neuhard, J.; Kelln, R.A.; Pedersen, S.
J. Bacteriol. 177, 517-523, 1995
J. Bacteriol. 177, 517-523, 1995
A.Fitle: The cmk gene encoding cytidine monophosphate kinase is located in the rpsA oper A; Reference number: 141019; MUID:95138007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Podbielski, A.
M.J. Gen. Genet. 237, 287-300, 1993
A.Title: Three different types of organization of the vir regulon in group A streptococc A. Reference number: 530283; MUID: 93204905
A. Rocession: 530284
A. Status: nucleic acid sequence not shown
A. Molecule type: DNA
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A; Residues: 1-436 <POD1>
A; Cross-references: EMBL.X88179

R; Cross-references: EMBL.X88179

R; Podbielski, A.; Melzer, B.
submitted to the EMBL Data Library, February 1991

A; Description: Por mediated cloning and sequencing of group A streptococcal emm41/52 (ev
A; Reference number: $29680

A; Accession: $29681
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C;Species: Streptococcus pyogenes
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C;Accession: S30284; S29681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA A;Molecule 158-248, DVRNTSVIVSPLVSKSLSSLRWSS', 251, 'SPL' <RES> A;Residues: 158-248, DVRNTSVIVSPLVSKSLSSLRWSS', 251, 'SPL' <RES> A;Cross-references: EMBL:X82933; NID:q599733; PIDN:CAA58106.1; PID:q599734 A;Experimental source: strain K-12; plasmid pSP547
                                                                                                                      Gaps
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                                                         Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 262;
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                                                             DB 2;
                                                      Score 39; DB;
Pred. No. 61;
3; Mismatches
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                                                      62.9%;
ilarity 57.1%;
Conservative
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77 KSSKYGKRLAKIAK 90
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77 KSSKYGKRLAKIAK 90
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Best Local Similarity
Matches 8; Conserv
                                                             Query Match
Best Local Similarity
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                                                                                                                Matches
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Gaps

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N. Alternate names: for V protein

C. Species: Streptococcus sp.

C. Accession: JG1419; S17354

R. Smirnov, O. Y.; Denesyuk, A. I.; Zakharov, M. V.; Abramov, V. M.; Zav'yalov, V. P.

R. Smirnov, O. Y.; Denesyuk, A. I.; Zakharov, M. V.; Abramov, V. M.; Zav'yalov, V. P.

R. Smirnov, O. Y.; Denesyuk, A. I.; Zakharov, M. V.; Abramov, V. M.; Zav'yalov, V. P.

R. Smirnov, O. Y.; Denesyuk, A. I.; Zakharov, M. V.; Abramov, V. M.; Zav'yalov, V. P.

R. Smirnov, O. Y.; Denesyuk, A. I.; Zakharov, M. V.; Abramov, V. M.; Zav'yalov, V. P.

A. Title: Protein V, a novel type-II IgG receptor from Streptococcus sp.: Sequence, A. Accession: JG1419

A. Septimental source: Strain 22/58'Valente'
C. Genetics:

A. Experimental source: strain 22/58'Valente'
C. Genetics:

A. Gene: Grv

C. Superfamily: M5 protein
C. Keywords: duplication; immunoglobulin receptor
C. Keywords: duplication; immunoglobulin repeat A
F: 209-303/Region: 35-residue repeat A
F: 339-373/Region: 35-residue repeat A
F: 339-373/Region: 35-residue repeat A
F: 346-450/Region: 35-residue repeat B
F: 416-450/Region: 35-residue repeat B
F: 416-450/Region:
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R: Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 159
A; Title: Non-congruent relationships between variation in emm gene sequences and the A; Reference number: $60802
A; Recession: $60802
A; Scatus: preliminary; nucleic acid sequence not shown; not compared with conceptual A; Molecule type: DNA
A; Rocelaides: 30-89 c/MA>
C; Superfamily: M5 protein
C; Keywords: coiled coil; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 539;
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JC1419
Fc gamma (IgG) receptor II precursor - Streptococcus sp.
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Pred. No. 1.2e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 2; 1
Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                               62.9%;
75.0%;
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Best Local Similarity 75.0%;
Matches 9; Conservative
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Matches 9; Conservative
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495 KLAKQAEELAKL 506
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447 KLAKQAEELAKL 458
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A; Residues: 1-539 <MOU>
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J. Bacteriol. 170, 676-684, 1988
A; Title: Molecular evolution of streptococcal M protein: cloning and nucleotide sequence
A; Reference number: A28549; MUID:88115166
A; Accession: A28549
A; Molecular type: DNA
                                                                                                                                                                                                                                                                    C; Species: Streptococcus sp.
A; Variety: group G
C; Date: 07-Sep-1994; #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C; Accession: 845599; 843554
R; ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoebring, U.
Biochem. 222, 267-276, 1994
A; Title: Streptokinase activates plasminogen bound to human group C and G streptococci
A; Reference number: 845598; MUID:94291620
A; Accession: 845599
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A;Status: preliminary
A;Status: 1-472 - 26E2>
A;Residues: 1-472 - 26E2>
A;Cross-references: EMBL:232678; NID:9474769; PIDN:CAA83589.1; PID:91333838
C;Superfamily: M5 protein
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C;Species: Streptococcus sp.
C;Species: Streptococcus sp.
C;Adet: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C;Accession: S54871
R;Podbielski, A.; Melzer, B.
Submitted to the EMBL Data Library, June 1991
A;Reference number: S54871
A;Reference number: S54871
A;Accession: S54871
A;Status: preliminary
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A;Variety: serotype M24
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 26-Aug-1999
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A;Residues: 1-53.2 <POD>*

A;Cross-references: EMBL.X60097; NID:g840905; PIDN:CAA42693.1; PID:g840906
C;Superfamily: M5 protein
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Pred. No. 1.1e+02;
2; Mismatches 1; Indels
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Pred. No. 1e+02;
2; Mismatches
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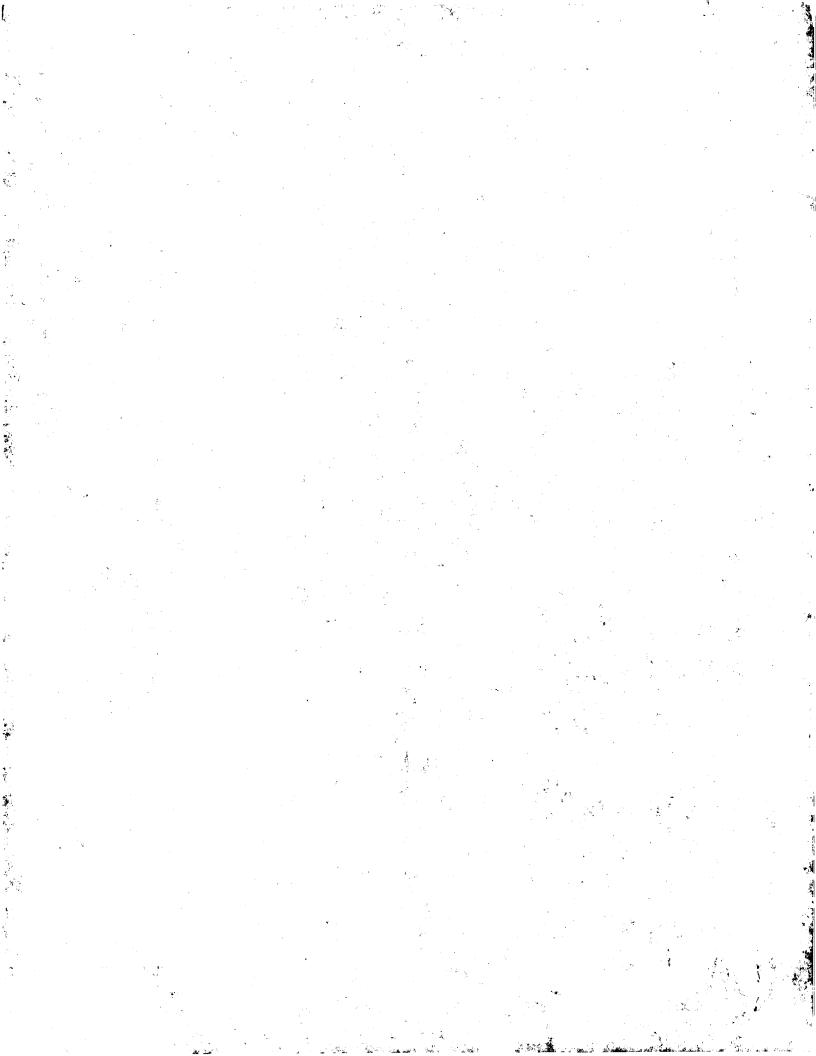
us-09-765-086-200.rpr

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A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630
A;Accession: C64071
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-142 < CTIGA
A;Residues: 1-142 < CTIGA
A;Residues: 1-142 < CTIGA
A;Cross-references: GB:032730; GB:L42023; NID:93212191; PIDN:AAC22136.1; PID:91573456; C;Superfamily: H+-transporting ATP synthase epsilon chain
C;Keywords: ATP blosynthesis; hydrolase; membrane-associated complex
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ó Gaps ö Query Match
61.3%; Score 38; DB 2; Length 142;
Best Local Similarity 72.7%; Pred. No. 50;
Matches 8; Conservative 3; Mismatches 0; Indels 2 LAKLAKKLAKL 12 :|||:|:||| 118 VAKLSKELAKL 128 ò

Search completed: May 8, 2002, 07:19:31 Job time: 99 sec

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SEQUENCE FROM N.A.
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ALIGNMENTS

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MEDLINE-82049532; PubMed-6271497;
Rothstein S.J., Jorgensen R.A., Yin J.C.P., Yong-Di Z., Johnson R.C., Reznikoff W.S.;
"Genetic organization of Tn5.";
Cold Spring Harb. Symp. Quant. Biol. 45:99-105(1981).
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MEDLINE=83050973; PubMed=6291786;
Johnson R.C., Yin J.C.P., Reznikoff W.S.;
Johnson F. Transposition in Escherichia coli is mediated by protein from the right repeat.";
Cell 30:873-882(1982).
                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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SEQUENCE OF 382-395 FROM N.A.
MEDLINE-83106478; Pubmed-6295884;
MEDLINE-83106478; Q., Auerswald E.A., Reiss B., Schaller H.;
Beck E., Ludwig G., Auerswald E.A., Reiss B., Schaller H.;
"Nucleotide sequence and exact localization of the neomycin phosphotransferase gene from transposon Tn5.";
Gene 19:327-336(1982).
                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A.
MEDLINE-82049482; PubMed=6271452;
Auerswald E.A., Ludwig G., Schaller H.;
"Structural analysis of Tn5.";
Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).
                                                                                      Last sequence update)
Last annotation update)
395 AA
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PRT;
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MEDLINE-81162719; Pubmed-6260374;
                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
PRELIMINARY;
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by a single base pair nonhomology.";
Cell 23:191-199(1981).
[6]
MEDLINE-83245055; PubMed=6306482;
                                                                                      Nature 304:280-282(1983)
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Rothstein S.J., Reznikoff W.S.; ^{\prime} The functional differences in the inverted repeats of Tn5 are caused
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MEDLINE-82049532; Pubmed-6271497;
Rothstein S.J., Jorgensen R.A., Yin J.C.P., Yong-Di Z., Johnson R.C.,
Reznikoff W.S.;
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MEDLINE-83050973; PubMed-6291786;
Johnson R.C., Yin J.C.P., Reznikoff W.S.;
"Control of Tn5 transposition in Escherichia coli is mediated laprotein from the right repeat.";
Cell 30:873-882(1982).
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                                                                                                           SEQUENCE FROM N.A. MEDLINE-83245055; PubMed-6306482; Johnson R.C., Reznikoff W.S.; "DNA sequences at the ends of transposon Tn5 required for
                                                                                                                                                                                                                                                                                                                                              Mobile DNA, pp.163-184, American Scolety for Microbiology Washington DC (1989).
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InterPro; IPR003201; Transposase_Tn5.
Pfam; PF02281; Transposase_Tn5; 1.
SEQUENCE 395 AA; 44757 MW; CBE32E0F62E84B8C CRC64;
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"Structural analysis of Tn5.";
Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).
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Cold Spring Harb. Symp. Quant. Biol. 45:99-105(1981)
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(In) Berg D., Howe M. (eds.);
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Rothstein S.J., Reznikoff W.S., \mbox{\sc "The functional differences in the inverted repeats of Tn5 are caused <math display="inline">\mbox{\sc "The functional differences in the inverted repeats of Tn5 are caused and the functional differences in the inverted repeats of Tn5 are caused in the functional differences in the inverted repeats of Tn5 are caused in the functional differences di
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Johnson R.C., Yin J.C.P., Reznikoff W.S.;
"Control of Tn5 transposition in Escherichia coli is mediated
protein from the right repeat.";
Cell 30:873-882(1982).
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Berg D.E.;

(In) Berg D., Howe M. (eds.);

Mobile DNA, pp.163-184, American Scoiety for Microbiology, Washington DC (1989).

EMBL; U00004; AAA7334.1; -.

InterPro: IPR003201; Transposase_Tn5.

Pfam; PFC2281; Transposase_Tn5.

Pfam; PFC2281; Transposase_Tn5.

SEQUENCE 421 AA; 47572 MW; D6C54358246F5D56 CRC64;
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Johnson R.C., Reznikoff W.S.; "DNA sequences at the ends of transposon Tn5 required for
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MEDIINE-82049482; PubMed-6271452;
Auerswald E.A., Ludwig G., Schaller H.;
"Structural analysis of Tn5.";
Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).
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MEDLINE-81162719; PubMed-6260374;
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Best Local Similarity 31.8%
Matches 7; Conservative
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SEQUENCE FROM N.A.
MEDLINE-82049532; PubMed=6271497;
Rothstein S.J., Jorgensen R.A., Yin J.C.P., Yong-Di Z., Johnson R.C.,
Reznikoff W.S.;
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MEDLINE-81162719; PubMed-6260374;
Rothstein S.J., Reznikoff W.S.;
"The functional differences in the inverted repeats of Tn5 are caused by a single base pair nonhomology.";
Cell 23:191-199(1981).
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MEDLINE=83050973; PubMed=6291786;
MCDLINE=83050973; PubMed=6291786;
Cohrson R.C., Yin J.C.P., Reznikoff W.S.;
"Control of Tn5 transposition in Escherichia coli is mediated by protein from the right repeat.";
Cell 30:873-882(1982).
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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(In) Berg D., Howe M. (eds.);
Mobile DNA, pp.163-184, American Scoiety for Microbiology,
Washington DC (1989).
EMBL; U00004; AAA73393.1; -.
EMBL; V00617; CAA23891.1; -.
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SEQUENCE 476 AA; 53304 MW; 737FA045F13D3D42 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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31.8%; Pred. No.
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MEDLINE-82049482; PubMed-6271452;
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                                    PRELIMINARY;
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(In) Berg D., Howe M. (eds.);
(In) Berg D., Howe M. (eds.);
Mobile DNA, pp.163-184, American Scoiety for Microbiology,
Washington DC (1989).
EMBL; 000004; AAA73388.1; -.
EMBL; V00615; CAA23888.1; -.
EMBL; V00615; CAA23888.1; -.
EMBL; V00615; Transposase_Tn5.
Pfam; PP02281; Transposase_Tn5.
Pfam; PP02281; Transposase_Tn5; 1.
SFOUENCE 450 AA; 50488 MW; C655574EA917A4C3 CRC64;
SEQUENCE FROM N.A.
MEDLINE-81245055; PubMed-6306482;
Johnson R.C., Reznikoff W.S.;
Juba sequences at the ends of transposon In5 required for transposition.";
Nature 304:280-282(1983).
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Structural analysis of Tn5.";
Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).
EMBL, 915572; AAB60063.1;
InterPro: IRR003201; Transposase_Tn5.
Pfam; PF02281; Transposase_Tn5.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Pred. No. 89;
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"The revised nucleotide sequence of Tn5.";
Gene 154:129-130(1995).
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MEDLINE-95172393; PubMed-7867940;
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STRAIN=PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                            2; Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.9%; Score 47; DB 2; Length 398; 30.4%; Pred. No. 1.7e+02; ive 15; Mismatches 1; Indels
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AE004541, AA64496.1; -.
InterPro; IPR00160; DUF9.
Pfam; PF00990; DUF9; 1.
SMART; SM00267; DUF1; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 398 AA; 44408 MW; 2A9C33E6AFA7CC79 CRC64;
                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHELICAL PROTEIN PA1107.
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Last annotation update)
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                      DB 7
                                                                                                                                                                                    398 AA
                                                        Mismatches
                            87.5%; Score 49; 31.8%; Pred. No.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
                                                                                                                                                                                    PRT;
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                                                        15;
                                                                                   23
                                                                                   2 MSIARLGGXXXXXXXXXXXX
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Best Local Similarity 30.4°
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
                                                        Conservative
                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
              Query Match
Best Local Similarity
T; Conserve
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CG2996.
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                                                                                                                                                                                                                                                                                                                   Pseudomonas
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                                                                                                                                                                                    0914M8
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                                           Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                      Auerswald E.A., Ludwig G., Schaller H.;

"Structural analysis of Tn5.";

Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).

EMBL, U15573; AAB66064.1; -.

InterPro: IRR003201; Transposase_Tn5.

Ffam: PF02281; Transposase_Tn5.

CONFLICT 200 200 K -> R (IN REF. 2).

CONFLICT 225 225 Y -> I (IN REF. 2).

CONFLICT 303 303 S -> G (IN REF. 2).

SEQUENCE 476 AA; 53306 NW; B52F2F143646AF10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASMID=PRL765;
Cai Y., Wolk C.P.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASMID=PRL1063A;
Wolk C.P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53314 MW; 83440E7A6220F8A2 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wolk C.P., Cai Y., Panoff J.M.;
Proc. Natl. Acad. Sci. U.S.A. 88:5355-5359(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 2
Pred. No. 95;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 AA
                                                                                                                                                        Ahmed A., Podemski L.;
"The revised nucleotide sequence of Tn5.";
Gene 154:129-130(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pRL765, and Plasmid pRL1063a.
Bacteria; environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR003201; Transposase_Tn5.
Pfam; PF02281; Transposase_Tn5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                             TRANSPOSON-TN5;
MEDLINE-95172393; PubMed-7867940;
                                                                                                                                                                                                                              TRANSPOSON=TN5;
MEDLINE=82049482; Pubmed=6271452;
                                                                                                                                                                                                                                                                                                                                                                                                                                              87.5%; Sco
31.8%; Pre
tive 15;
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Best Local Similarity 31.00
Best Local 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 AA;
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SEQUENCE FROM N.A.
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                                                                       Escherichia.
NCBI_TaxID=562;
                          TRANSPOSASE.
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SEQUENCE
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Q57047;
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Gaps

Matches

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Gaps

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67 SMSAAKIGGGMVQTGQTLGTIKV 89

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Winstanley C., Hales B.A., Corkill J.E., Gallagher M.J., Hart C.A.; "Flaggellin gene variation between clinical and environmental isolates of Burkholderia pseudomallei contrasts with the invariance among
                                                                                                                                                                                                                                                                                                                                                Winstanley C., Hales B.A., Corkill J.E., Gallagher M.J., Hart C.A.; "Flagellin gene variation between clinical and environmental isolates of Burkholderia pseudomallei contrasts with the invariance among clinical isolates."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLAGELLIN (FRAGMENT).

Burkholderia, Proteobacteria; beta subdivision; Burkholderia group;

Burkholderia.
                                                                                                                                FLAGELLIN (FRACMENT).
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.1%; Score 46; DB 2; Length 249; 26.1%; Pred. No. 1.4e+02; tive 16; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AA; 24915 MW; EFF4C8CA527174C3 CRC64;
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254 AA; 25363 MW; 7EEE33271B33BA71 CRC64;
                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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               249 AA
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EMBL; AF030241; AAC27443.1; -.
InterPro; IPR001029; Flagellin_C.
ProDom; PD000316; Flagellin_C; 1.
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J. Med. Microbiol. 47:689-694(1998).
EMBL. AF030240; AAC27442.1;
InterPro: IPR001029; Flagellin_C.
Probom; PD000316; Flagellin_C: 1.
               PRT;
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MEDLINE=99093016; PubMed=9877189;
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MEDLINE=99093016; PubMed=9877189;
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Best Local Similarity 20....
6; Conservative
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               PRELIMINARY;
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Matches 6; Conserva
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NON_TER
SEQUENCE
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SEQUENCE
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Q9R9B1;
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Rodorge R.A., Lewis S.E., Richards S., Ashburnera M., Henderson S.N.,
Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Ann K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Haltoo G.L.G.,
Aban K.H., Obole C., Baxter E.G., Helf G., Nelson C.R., Haltoo G.L.G.,
Ballay R.M., Basu A. Baxendale J., Baytaktarogu L., Beasley E.M.,
Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Aberry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
Ab Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
Ab Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
Ab Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
Ab Codon K., Doup L.E., Downes M., Davies M.,
A Godon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.
Brandlin K.J., Harvey D., Heilman T.J., Hernandez J.R., Harris M.L.,
A Hostin D., Houston K.A., Harvey D., Heilman T.J., Hernandez J.R., Harris M.L.,
A Hostin D., Houston K.A., Lewinsky R.A., Li J., Mei M.-H., Ibegwam C.,
Alalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalali M., Malthan N.V., Mobarry C., Morins J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Shue B.C., Siden-Kiamos I., Simpson M., Stuong K., Sun E.,
Syler E., Spradling A.C., Stapleton M., Stuong R., Sun R.,
Syler E., Spradling A.C., Stapleton M., Stuong R., Sun R.,
Syler E., Spradling A.C., Stapleton M., Stuong S., Yao Q.A.,
Wang Z.-Y., Wassarman D.A., Welbartock G.M., Welssenbach J.,
Whyer B., Woodage T., Worley K., Wu D., Yang S., Yao Q.A.,
Syler E., Spradling A.C., Stapleton M., Stuong S., Yao Q.A.,
Annelson D.R., Wadosgorinia melanogaster.", Smith H.O.,
Rhilams S.M., Woodage T., Worley W., Wu D., Yang S., Yao Q.A.,
Sheng X.H., Zhong F.N.
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SEQUENCE 4215 AA; 470517 MW; 53613E810BA8D4F1 CRC64;
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SMART; SM00179; EGF CA; 2.
SMART; SM00010; EGF_LIKe; 6.
PROSITE; PS00010; ASX_HVDROXYL; 2.
PROSITE; PS01180; CUB; 29.
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PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01187; EGF_CA; 3.
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Best Local Similarity
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Gaps

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Q9WWT2 O9WWT2

RESULT 12 09WWT2

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PROUNT FROM N.A.

SEQUENCE FROM N.A.

STRAIN=DMS 3027, DMS 2555;

A Tungpradabkul S., Wajanarogana S., Tunpiboonsak S., Panyim S.;

Tungpradabkul S., Wajanarogana S., Tunpiboonsak S.,

Tungpradabkul S., Wajanarogana S.,

Tungpradabkul S., Wajanarogana S., Tunpiboonsak S.,

Tungpradabkul S., Wajanarogana S.,

Tungpradabkul S., Wajanarogana S.,

Tungpradabkul S., Panyim S.;

Tungpradabkul S.,

Tungpradab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brett P.J., Woods D.E.;
"Vaccine Strategies for Immunoprophylaxis Against Melioidosis.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF081500; AAC31966.1; -
InterPro; IPR001029; Flagellin_C.
InterPro; IPR001492; Flagellin_N.
                                                                                                                                                                                                                                                                                                                                                                             Burkholderia thailandensis.
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLAGELLIN (FRAGMENT).
Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.1%; Score 46; DB 2; Length 383; 26.1%; Pred. No. 2.5e+02; tive 16; Mismatches 1; Indels
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Pfam: PF00700; Flagellin_C: 1.
PRINTS: PR00207; FLAGELLIN.
PRODOM: PD000316; Flagellin_C: 1.
SEQUENCE 383 AA; 38809 MW; 64D681308F690399 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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ProDom; PD000316; Flagellin_C; 1.
NON_TER 383 383
                                    163 SMSAAKIGGGLVQFGQTLGTFKV 185
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1 SMSIARLGGXXXXXXXXXXXX 23
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Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=E264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=57975;
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NCBI_TaxID=292;
                                                                                                                                                                                                                                                                                                                             FLAGELLIN.
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086045;
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Q9Z3A8
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Wajanarogana S., Tungpradabkul S., Panyim S.;
Wajanarogana S., Tungpradabkul S., Panyim S.;
Wariation of flagellin genes between virulent and non-virulent
T strains of Burkholderia pseudomallel.";
Lubmitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF078153; AAD24678.1;
R interPro; IPR001029; Flagellin_N.
F fam; FF007069; Flagellin_N.
R PF007069; Flagellin_C:
R PRINTS; PR00207; FLAGELLIN.
R PRODOM; PD00316; Flagellin_C:
T NON TER 382 A8; 38681 MW; F681308F690399IF CRC64;
                                                                                                                                                                                                                                                                                                                                                                          STRAIN-E 276;
Wajanzrogana S., Tungpradabkul S., Panyim S.;
Wajanzrogana S., Tungpradabkul S., Panyim S.;
Wariation of flagellin genes between virulent and non-virulent strains of Burkholderia pseudomallel.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ARO78155; AAD24680.1;
InterPro; IPR001029; Flagellin_C.
InterPro; IPR001492; Flagellin_N.
Pfam; PF00669; Flagellin_N; 1.
                                                                                                                                                                                                             Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
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Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.1%; Score 46; DB 2; Length 382; 26.1%; Pred. No. 2.5e+02;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                  PRT;
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Probom; PD000316; Flagellin_C; 1.
NON_ITS 3820110, C; 1.
SEQUENCE 382 AA: 38690 MW; 68:
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098640

RESULT 13 098640

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Gaps

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SQ SEQUENCE 383 AA; 38657 MW; 1B53B946EA01070E CRC64;
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; 0 0; Gaps Query Match 82.1%; Score 46; DB 2; Length 383; Best Local Similarity 26.1%; Pred. No. 2.5e+02; Matches 6; Conservative 16; Mismatches 1; Indels

Search completed: May 8, 2002, 07:29:58 Job time: 111 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 8, 2002, 07:28:07 ; Search time 12.9 Seconds (without alignments) 65:371 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Ď,		P40713		P55849			028069	P26420	P26984					P12024	09pep8	P26161		P22441	P56346	O9mum5	P12437	. P15003	011016	028105	P74227	. 051	P35583	P45632	Q9z114		Q25414 lymnaea sta	Q9uk80	
SUMMARIES	ID	MEFD	SCRK_ECOLI	V50K_BYDVP	DSC1_MOUSE	YLK3_CAEEL	PAAD_AERPE	YM14_ARCFU	SCRK_KLEPN	SCRK_SALTY	YDJE_BACSU	IMDH_METJA	RIR1_BACSU	YS8A_CAEEL	CHAO_DROME	COAD_XYLFA	YPU5_RHOCA	RPC1_LAMBD	DHMA_FLAS1	MIND_CHLVU	MIND_MESVI	PERX_SOLTU	PER1_LYCES	YD46_MYCTU	YL78_ARCFU	EFTU_SYNY3	CLPX_BORBU	HN3B_MOUSE	EXOC_AZOBR	IMDH_HELPJ	IMDH_HELPY	5HT_LYMST	UBPN_HUMAN	DISTON MOUTH
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de	Query Match	82	0	80.4	٠	ö	ω.	ω.	78.6	æ	œ.	ω.	æ	æ	æ	ė.	ė	ė.	ė	ė.	ė.	76												
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1 YD54_MYCTU	ALIGNMENTS	Ю; РRT; 498 AA.	01-30-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) MYCCYTE-SPECIFIC ENHANCER FACTOR 2D HOMOLOG (SERUM RESPONSE FACTOR- LIKE PROTEIN 1) (SL-1).	Menopus laevis (African clawed frog). Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Menopodinae; Xenopus. NOBL_TAXID=8355;	[1] TISSUE-Neurula; MEDLINE-93099873; PubMed=1281451; Chambers A.E., Kotecha S., Towers N., Mohun T.J.; "Muscle-specific expression of SRF-related genes in the early embryo	SPECIFIC TRANSCRI RIPTION OF A VARI SEQUENCE CTA(T/A). MER, PROBABLY AS A	SUBCELLUTAR LOCATION: NUCLEAR. ISSUE SPECIFICITY: RESTRICTED TO THE SOMITIC MESODERM OF EARLY EMBRYOS AND TO THE BODY MUSCLE (MYOTOMES) OF THE TADPOLE. EXPRESSED IN ALL TISSUES EXAMINED IN THE ADULT. BEVELOPMENTAL STAGE: EXPRESSION BEGINS IN THE LATE GASTRULA. SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS. MEF2 SUBFAMILY.	SWISS-PROT entry is copyright. It is produced through a collaboration seen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fied and this statement is not removed. Usage by and for commercial ties requires a license agreement (see http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).	EMBL; Z19124; CAA79531.1; HSSP; P11831; 1SRS. InterPro; 1PR001210; MADS-box. Pfam; PF00319; SRF-TF; 1. PRINTS; PR00404; MADSDOMAIN. SMART; SM00432; MADS; 1. PROSITE; PS00350; MADS_BOX_1; 1. PROSITE; PS00056; MADS_BOX_2; 1. Transcription regulation; Nuclear protein; DNA-binding; Activator; Multigene family. DOMAIN 58 86 MEE2-TYPE (POTENTIAL).	
623 76623 9889 9899 1093 3005 7008		STANDARD;	35, C 35, L 37, L ENHANC SL-1).	frican a; Cho ia; An pus.	PubMe recha expres	PEGUL REGUL Y REGU IT BI	OCATIO ICITY: O THE ALL TI STAGE	ntry is Inst. Information it in state a lictory	7.9531. S.S. MADSDO MADSDO MADS, 1 MADS MADS MADS MADS MADS MADS MADS MADS	31
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40000000000000000000000000000000000000		T 1 XENLA MEFD_XENLA	01-NOV-1997 01-NOV-1997 15-DEC-1998 MYOCYTE-SPE LIKE PROTEI	Xencous lacris (African clawed Xencous Bukaryota; Metazoa; Chordata; o Amphibia; Batrachia; Anura; Mes Xencopodinae; Xencous.	til SEQUENCE FROM N.A. TISSUE=Neurula; MEDLINE=93099873; Chambers A.E., Kot "Muscle-specific e	of Xenopus EMBO J. 11: -!- FUNCTIC EMBRYO IN THE	- 1 - SUBCELI - 1 - TISSUE EMBRYOS - 1 - DEVELOR - 1 - SIMILAR - 1 - SIMILAR	This SWISS-between the Europeause by no modified an entities re	EMBL, 21912 HSSP, P1183 HTGFPRO; J Pfam; PF003 PRINTS; PRC SMART; SMC PROSITE; PE PROSITE; PE Transcripti Multigene f DOMALIN	
www.www.a4444 4706/2000-110440		SUI.		5800088				8888888888		

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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DSC1_MOUSE
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                                                            Gaps
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01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
50 Rel. 16, Last annotation update)
50 Rel. 10 Marf 41.
51 Rel. 10 Marf 41.
52 Rel. 10 Marf 41.
53 SERNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                      Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
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                                        Length 498
                                                            Indels
        9E98D13D80AAF510 CRC64;
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SEQUENCE 305 AA; 33081 MW; 5F9C8D59B66C3E55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                        DB 1;
                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
FRUCTOKINASE (EC 2.7.1.4).
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                                                          15; Mismatches
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                                        Score 46;
 GLN-RICH
                                                Pred. No.
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PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
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                                                                              2 MSIARLGGXXXXXXXXXXX 23
          54071 MW;
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                                       82.18;
ilarity 27.38;
Conservative 1
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Best Local Similarity
        498 AA;
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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P09516;
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P40713;
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          SEQUENCE
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-! INVEST. DETMATO1. 107:531-538(1996).

-! FUNCTION: COMPONENT OF INTERCELLUIAR DESMOSOME JUNCTIONS. INVOLVED
IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
MEDIATING CELL.-CELL ANGESION. MAY CONTRIBUTE TO EPIDERMAL CELL
POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL
ADHESIVENESS BETWEENER CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED
TO THE KERATINIZATION OF EPITHELIAL TSSUES.
-! SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.
-! ALTERNATIVE PRODUCTS: Z ISOFORMS; IA (SHOWN HERE) AND 1B; ARE
PRODUCED BY ALTERNATIVE SPLICING.
-! DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
SEQUENCE FROM N.A.

MEDLINE-88289355; PubMed=3399386;

Miller W.A., Waterhouse P.M., Gerlach W.L.;

"Sequence and organization of barley yellow dwarf virus genomic RNA.";

Nucleic Acids Res. 16:6097-611(1988).

-! SIMILARITY: TO ORE 6 OP BEET WESTERN YELLOWS VIRUS, ORF6 OF

POTATO LEAFROLL VIRUS AND OF 54K PROTEIN OF BEET NECROSIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 King I.A., O'Brien T.J., Buxton R.S.; "Expression of the 'skin-type' desmosomal cadherin DSC1 is closely linked to the keratinization of epithelial tissues during mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002929; PLRV_ORF5.
Pfam; PF01690; PLRV_ORF5; 1.
SEQUENCE 450 AA; 49733 MW; 5878FA9361498205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DESMOCOLLIN 1A/18 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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MEDLINE-96420658; PubMed-8823356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X07653; CAA30495.1; -.
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                                                                                                                                                                                                                                                                           YELLOW VEIN VIRUS.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY). ATP (BY SIMILARITY).
modified and this statement is not removed. entities requires a license agreement (See h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 AA
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                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SMSIARLGGXXXXXXXXXXX 23
                                                            EMBL; U00065; AAA50735.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                           461 46
569 56
1895 AA;
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Matches 6; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aeropyrum.
NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAAD_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K1;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pauley A., Waterston R.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
STRONG, TO ZC84.1.
-!- SIMILARITY: CONTAINS ? EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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              entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
N-LINKED (GLCNAC. . .) (POTENTIAL).
KVILCGQAEEH -> ESIRGHTLIKN (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3 IN CHROMOSOME III
                                                                                                                                                                                    PROSITE; PS00232; CADHERIN_1; 2.
PROSITE; PS50268; CADHERIN_2; 4.
Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein; Calcium-binding; Repeat; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
 Usage by
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN ISOFORM 1B).
F34F8D8578CE92F7 CRC64;
                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.4%; Score 45; DB 1; I 26.1%; Pred. No. 1.7e+02; tive 15; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1895 AA.
 and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                              CADHERIN 1.
                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                          EMBL, X97986, CAA66628.1; -.
EMBL, X97986, CAA66629.1; -.
HSSP, P09981, IEDH.
MGD, MGI:109173; DSG1.
InterPro; IPR002126; Cadherin.
Pfam, PF00028; Cadherin. 5.
PRINTS; PR00226; Cadherin.
SMART; SM00112; CA: 4.
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nes 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
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130
165
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P41951;
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DOMAIN
TRANSMEM
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CARBOHYD
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noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                           R HSSP; Q63450; 1A06.

R WormPep; D1044-3; CE01206.

R InterPro; IPR000561; EGF-1ike.

R InterPro; IPR000561; EGF-1ike.

R InterPro; IPR000519; EBL.pkinase.

R InterPro; IPR00059; Ser_thr_kin_actsite.

R Ffam; PF00069; PKinase; 1.

R PRART; SM00220; STKC; 1.

R SMART; SM00289; WR1; 12.

R PROSITE; PS00110; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS0111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crenirchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(199).
-!- SIMILARITY: BELONGS 10
PHENYLACRYLLC ACID DECARBOXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.4%; Score 45; DB 1; Length 1895; 26.1%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 BY SIMILARITY.
208393 MW; F23C9F7881353AD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE AROWATIC ACID DECARBOXYLASE (EC 4.1.1.-).
APE1647.
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EMBL; AP000062; BAA80648.1; -.

SO WE DR SO

028069 YM14_ARCFU

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -: - SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.6%; Score 44; DB 1; Length 307; 21.7%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32343 MW; F8CB20B234B262FA CRC64;
                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
FRUCTOKINASE (EC 2.7.1.4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Mismatches
                                                                                                                     307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002173; PfkB. Pfam; PF00294; pfkB; 1.
                                                                                                                                                                                                                                                               FRUCTOKINASE (EC 2.7.1.4).
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                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                              Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; $16037; $16037.
PIR; $18523; $18523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=602;
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                                                                                                                                                                                                                                                                                                                                                                                    Klebsiella.
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                                                                                                                     SCRK_KLEPN
P26420;
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P26984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
SCRK_SALTY
                                                               σ
                                                                                             SCRK_KLEPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCRK.
                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlaraye A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G. (311 S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., MoNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the hyperthermophilic, sulphatereducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-i. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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InterPro; IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein. 1.
Hypothetical protein; Lyaschoxylase; Complete proteome.
SEQUENCE 197 Ast, 21184 MW; BB878C6DB14C4B7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.6%; Score 44; DB 1; Length 221; 28.6%; Pred. No. 55; 1ive 15; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                              78.6%; Score 44; DB 1; Length 197 22.7%; Pred. No. 48;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
888043795312594C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN AF2214.
                                                                                                                                                                                                                                    17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                 163 PO
200 PO
24925 MW;
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                                                                                                                                                                                                                                                                                                2 MSIARLGGXXXXXXXXXXX 23
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Best Local Similarity 28.5%
                                                                                                                                                                                                         Local Similarity 22.7% nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C.;
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SEQUENCE
                                                                                                                                                                                 Query Match
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GUAB OR MJ1616.
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                                                                                                                                                                                                                                                                                                                                                                            Methanococcus
                                                                                                                                                                                                                                                                       01-NOV-1997
                                                                                                                                                                                                                                                 IMDH_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jannaschii
                                                                                                      Query Match
                                                                                                                                                                                                                                                             059011;
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                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the FMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                 -1- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
            MEDLINE-92236409; PubMed-1809835;
Aulkemeyar P., Ebner R., Hellenmann G., Jahreis K., Schmid K.,
Warieden S., Lengeler J.W.;
"Molecular analysis of two fructokinases involved in sucrose
                                                                           Mol. Microbiol. 5:2913-2922(1991).
-!- CATALYTIC ACTIVITY: ATP + D-FRUCTOSE = ADP + D-FRUCTOSE
                                                                                                                                                                                                                                                                                                                                                                                          78.6%; Score 44; DB 1; Length 307; 21.7%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL SUGAR KINASE IN GUTA-COTA INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                        ;; Kinase; Plasmid.
307 AA; 32916 MW; E01CB770CE20B329 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                            Pfan; PF00294; pfkB; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168 / MARBURG;
MEDLINE=98116660; PubMed=9455482;
                                                               metabolism of enteric bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SMSIARLGGXXXXXXXXXXX 23
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                                                                                                                                                                                                                                            EMBL; X61005; CAA43323.1; -. PIR; S16044; S16044. PIR; S18524. InterPro; IPR002173; PfkB.
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                   6-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                         ransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDJE OR FRUC
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034768;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDJE_BACSU
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-1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION OF CELL GROWTH (BY SIMILARITY).
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MEDLINE-96337999; PubMed=86808087;

MEDLINE-96337999; PubMed=8688087;

Bull C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A. Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Raich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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XANTHOSINE 5'-PHOSPHATE + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205) (IMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 320;
InterPro; Iranova...;
Pfam; PP00294; pfkB; 1.
PROSITE; PS00584; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
Hypothetical protein; Transferase; Kinase; Complete profigorial pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Mismatches
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InterPro; IPR003009; FMN_enzyme.
InterPro; IPR01093; IMP_DH_GMP_RED.
Pfam; PF00571; CBS; 2.
Pfam; PF00478; IMPDH_C; 1.
Pfam; PF01574; IMPDH_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEHYDROGENASE) (IMPDH) (IMPD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U67602; AAB99638.1; -. HSSP; P50097; 1AK5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMP REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2190;
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78.6%; Score 44; DB 1; Length 700; 21.7%; Pred. No. 2e+02;

9

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Best Local Similarity
Matches 5; Conserv
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                               009625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
CHAO_DROME
                                                                                                                                   YS8A_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-97124182; Pubmed-8969495; Scotti C., Valbuzzi A., Perego M., Galizzi A., Albertini A.M.; The Bacillus subtilis genes for ribonucleotide reductase are similar to the genes for the second class I NrdE/NrdF enzymes of Enterobacteriaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MICTOBIOLOGY 142:2995-3004(1996).
-!- FUNCTION: CATALYZES THE BIOSYNTHESIS OF DEOXYRIBONUCLEOTIDES FROM THE CORRESPONDING RIBONUCLEOTIDES, PRECURSORS THAT ARE NECESSARY FOR DNA SYNTHESIS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE DIPHOSPHATE + OXIDIZED THIOREDOXIN + H(2)0 = RIBONUCLEOSIDE DIPHOSPHATE + REDUCED
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE
LARGE CHAIN FAMILY. MORE SIMILAR TO ENTEROBACTERIAL NRDE THAN TO
           PROSITE; PS00487; IMP_DH_GMP_RED; 1.
Oxidoreductase; NAD; GMP blosynthesis; Purine blosynthesis; Repeat;
CBS domain; Complete proteome.
DOMAIN 43 95 CBS 1.
                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: FIRST REACTION IN THE DNA REPLICATION PATHWAY. SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
                                                                                                                                Score 44; DB 1; Length 496;
Pred. No. 1.4e+02;
8; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subtilist; BG11404, nrdE.
InterPro; IPR000788; Ribonucleo_red.
Pfam; PF00317; ribonucleo_red; 1.
PROSITE; PS00089, RIBORD_LARGE; 1.
Oxidoreductase; DNA replication; Complete protecome.
SEQUENCE 700 AA; 80688 MW; D2D4B914B97BBFA6 CRC64;
                                                                              IP (POTENTIAL).
C3E03FDDF3898396 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                  700 AA.
                                                                                                                             CBS 1.
CBS 2.
                                                                                                                                                                                                                                                                                  PRT;
                                                                              IMP
                                                                                                                                                                                                         61 AIALARLGGLGVIHRNMSIEEQV 83
                                                                                                                                                                                       1 SMSIARLGGXXXXXXXXXXX 23
                                                                                           53316 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z68500; CAA92810.1; -. EMBL; Z99113; CAB13622.1; -.
                                                                                                                                              Local Similarity 21.7% nes 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                 (RIBONUCLEOTIDE REDUCTASE)
                                                                                                                                                                                                                                                                                  STANDARD;
 CBS; 2.
                                                                  155
                                                                              306
                                                    43
103
306
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
 SM00116;
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                                                                                                                                                                                                                                                                                                                                                                                 NRDE OR NRDA
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P50620;
                                                                DOMAIN
BINDING
SEQUENCE
                                                                                                                                   Query Match
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P12024, 09VAD.;
01-0CT-1989 (Rel. 12, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2011 (Rel. 40, Last annotation update)
20-AUG-2011 (Rel. 40, Last annotation property PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN).
CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN).
CHO OR CHT OR CG1744.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
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0
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Indels
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                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 84.3 KDA PROFEIN ZK945.10 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilkinson-Sproat J.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76DC5B03E6357A6A CRC64;
ä
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26.1%; Pred. No. 2.3e+02;
                                                                                                                                                                                                               796 AA.
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SER/THR-RICH.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Transmembrane
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 248582; CAA88469.1; -.
EMBL; 248544; CAA88446.1; JOINED.
EMBL; 248544; CAA88444.1; -.
EMBL; 248582; CAA88444.1; JOINED.
WORTHPEP; ZK945.10; CE01732.
                                                                          189 SMOLSKLGGGVSLNLSKLRAKGE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          609 SVSMPRLGGTYPASTFVGPGNYT 631
                                               1 SMSIARLGGXXXXXXXXXXXX 23
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                           ZK945.10.
Caenorhabditis elegans.
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546
752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                    YS8A_CAEEL
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RC STRAIN—EBERKELEY,
RM MEDINE—2010-80065, Pubked—10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutron G.G., Worthman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H.C., Blazej R.G., Channe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Besson R.Y., Baxendal J., Bayraktarolyl L., Beasley E.M.,
RA Besson R.Y., Baxendal B.P., Bhandari D., Bolshakov S.,
RA Burtis R.C., Busam D.A., Bultler H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davemport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Ballke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Burtis R.C., Gabrieliata C.C., Ferraz C., Ferriard S., Pleischmann W.,
RA Gong F., Gorrell J.H., Gu Z., Gaun P., Harris M.,
RA Hostin D., Houston R.A., Heiman T.J., Well M.-H., Thegwam C.,
Alabli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchm K.A.,
RA Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A.,
Moult S.M., Moy M., Morrhy B., Morpherson D.,
RA Merkulov G., Milshina N.Y., Mixon K., Musskern D.R., Pacled J.M.,
Rabon D.R., Pittuan G.S., Pan S., Pollard J., Puti Y., Reese M.G.,
Reinert K. Remington K.A., Ronson M., Strong R., Such B.,
Syltskas R., Tector C., Turner R., Venter E., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock S., Cheeler F., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock S., Cheeler F., Rang S., Pollard J., Russ R.,
Rainer S.M., Woodage T., Singson M., Strong S., Zhu X., Smith H.O.,
Raber R., Penner G. Worley G., Shong S., Zhu X., Shon H.,
Raber R., Penner S.W., Rubin G.M., Venter J.C.;
R., Schence S.B., Schence S. Bong S., Zhu X., Shith H.O.,
R., Penner R., Penner G., Shider S., Shong S., Schence S., Shong S., Schence S., Shong S., Schence S., Shong S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zipursky S.L., Venkatesh T.R., Teplow D.B., Benzer S.; "Neuronal development in the Drosophila retina: monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL MORPHOGENESIS. MEDIATES HOMOPHILIC CELLULAR ADHESION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zipursky S.L., Venkatesh T.R., Benzer S.;
"From monoclonal antibody to gene for a neuron-specific glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: EXPRESSED IN PHOTORECEPTOR CELLS AND THEIR AXONS IN THE ADULT RETINA, THE OCELLUS AND LARVAL PHOTORECEPTOR
                MEDLINE=88135762; PubMed=3124963;
Reinke R., Krantz D.E., Yen D., Zipursky S.L.;
"Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cell morphogenesis, contains a repeat motif found in yeast and human.";
Cell 52:291-301(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: EXTRACELLULAR SURFACE OF R-CELL PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: EXPRESSED 24 HOURS AFTER INITIATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in Drosophila.";
Proc. Natl. Acad. Sci. U.S.A. 82:1855-1859(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 30-50, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CANTON-S; TISSUE-Head; MEDLINE-84106810; PubMed-6420071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Head;
MEDLINE=85166231; PubMed=3920657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 30-50 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as molecular probes.";
Cell 36:15-26(1984).
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEMBRANE
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PHOTORECEPTOR CELL DIFFERENTIATION, PERSISTS THROUGH DEVELOPMENT
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-!- SIMILARITY: BELONGS TO THE CHAOPTIN FAMILY. -!- SIMILARITY: CONTAINS 38 LEUCINE-RICH REPEATS (LRR). -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 1123.

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InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam., PF00560; LRR_typ.
SMART; SM00370; LRR; 4.
SMART; SM00369; LRR; 4.
Glycoprotein; Membrane; Signal; Repeat; Leucine-rich repeat; Vision.
SIGNAL EMBL, M19017; AAA28425.1; ALT_FRAME.
EMBL, M19008; AAA28425.1; JOINED.
EMBL, M19010; AAA28425.1; JOINED.
EMBL, M19010; AAA28425.1; JOINED.
EMBL, M19011; AAA28425.1; JOINED.
EMBL, M19012; AAA28425.1; JOINED.
EMBL, M19013; AAA28425.1; JOINED.
EMBL, M19014; AAA28425.1; JOINED.
EMBL, M19016; AAA28425.1; JOINED.
EMBL, AE003777; AAE57127.1; -. PIR; A29944; A29944. FIYBASS: FBGN0000313; chp. INTEPPRO; IPR000225; Armadillo. INTERPO; IPR001611; LRR.

30 101 126 1150 1175 1199 224 224 249 277 3302 349 CHAIN REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT

12. 13. 14. 15. 17. 17. 17. 17. 17. 17. 44433 4444 REPEAT

REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT

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Gaps
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20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHOPANTETHEINE ADENYLYLTRANSFERASE (EC 2.7.7.3) (PANTETHEINE-PHOSPHATE ADENYLYLTRANSFERASE) (PPAT) (DEPHOSPHO-COA
                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                           (POTENTIAL).
                                                                                                                          (POTENTIAL)
                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                         (POTENTIAL)
                                                              POTENTIAL)
                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                   78.6%; Score 44; DB 1; Length 1315; 26.1%; Pred. No. 4.1e+02; ative 16; Mismatches 1; Indels
                                                                                                                                                                                             D2D89A64EB46FCE5 CRC64;
                                                           N-LINKED GLCNAC...)
                                              (GLCNAC
                                                      (GLCNAC
                                                                                                                                                                                                                                                                                                       162 AA
LRR 35.
LRR 36.
LRR 37.
LRR 38.
N-LINKED
                                             N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=9A5C;
MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                            1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Created)
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                                                                                                                                                                                                           Query Match
Best Local Similarity 20.1.
Best Conservative
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                                                                                                                                                                                                                                                                                                                                                                  COAD OR XF0980.
Xylella fastidiosa
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8, 2002, 07:30:47

Search completed: May Job time: 160 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                   PHOSPHOPANTETHEINE, YIELDING DEPHOSPHO-COA (DPCOA) AND PYROPHOSPHATE (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP + PANTETHEINE 4'-PHOSPHATE = DIPHOSPHATE DEPHOSPHO-COA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                     -!- FUNCTION: REVERSIBLY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A. Jr., de Souza A.D., Terenzi M.L.Z., Siqueira W.J. de Souza A.A., de Souza A.P., Silvestri M.L.Z., Siqueira W.J., de Souza A.R., Varlada H.P., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Nucleotidyltransferase; Coenzyme A biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.8%; Score 43; DB 1; Length 162; 30.0%; Pred. No. 58; ive 14; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   -i- PATHWAY: COENZYME A (COA) BIOSYNTHESIS; FOURTH STEP.
-i- SUBDINIT: HOWOHERAMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE COAD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA; 17568 MW; 519E4052D4E364FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001980; LPS_biosynth.
InterPro; IPR001994; Cytidylyltransf.
Pfam; PF01467; Cytidylyltransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003936; AAF83790.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 IARLGGDVSGFAPAAVVAAL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01020; LPSBIOSNTHSS
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Best Local Similarity
Matches 6; Conserv
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         δ
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Wed May 8 07:50:31 2002

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 8, 2002, 07:28:07; Search time 22.67 Seconds (without alignments) 77.283 Million cell updates/sec

CHIMERA_X 56 1 SMSIARLGGXXXXXXXXXXXXX 23 Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database:

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| SUMMAKIES | Description | conserved hypothet | serum response fac | Arm repeat contain | hypothetical prote | probable fructokin | fructokinase XF161 | probable fructokin | probable membrane | 24 | hypothetical 49.8K | | | conserved hypothet | conserved hypothet | hypothetical prote | hypothetical prote | | hypothetical prote | hypothetical prote | conserved hypothet | ribonucleoside-dip | D-fructokinase [im | | fructokinase (EC 2 | fructokinase homol | hypothetical prote | ne transp | IMP dehydrogenase | TOTAL DI HERONA |
|-----------|----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|-----------|-------------------|-----------------|
| SUMM | ΙD | D83506 | S28059 | T47846 | C83338 | S52161 | B82660 | 689965 | E64822 | A85595 | JQ1419 | 800950 | T33240 | F83100 | E81706 | T15881 | C75510 | C72545 | T25975 | B84035 | F69526 | H69926 | C85878 | S18523 | S18524 | A69789 | F72552 | S60897 | G64501 | B84782 |
| | DB | 7 | 7 | 7 | ~ | Н | 7 | 7 | - | 7 | 7 | 7 | 7 | 7 | 7 | 7 | ~ | ~ | 7 | 7 | ~ | 7 | ~ | | - | 7 | 7 | 7 | - | ~ |
| | Length | 398 | 498 | 928 | 283 | 305 | 338 | 384 | 402 | 402 | 449 | 450 | 598 | 687 | 826 | 1895 | 131 | 197 | 208 | 211 | 221 | 240 | 305 | 307 | 307 | 320 | 391 | 431 | 496 | 672 |
| di | Query
Match | 83.9 | 82.1 | 82.1 | 80.4 | 80.4 | 80.4 | 80.4 | 80.4 | 80.4 | 80.4 | 80.4 | 80.4 | 80.4 | 80.4 | 80.4 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 |
| | Score | 47 | 46 | 46 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 45 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 |
| | Result
No. | П | 7 | က | 4 | S | 9 | 7 | œ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 |

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| conserved hypothet ribonucleoside-dip | hypothetical prote
ribunucleotide red
chaoptin precursor | hypothetical prote hypothetical prote | hypothetical prote hypothetical prote | membrane transloca
lipopolysaccharide
hypothetical prote | repressor protein hypothetical prote N-acylmannosamine | cell division inhi |
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B69667 | T21460
T12925
A29944 | E85649
S76238 | T21052
A72685 | T48528
C82738
S17807 | RPBPL
G85513
A43744 | T07303 |
| 0.0 | 777 | 0 0 | 7 7 | 0 0 0 | 124 | 7 |
| 685 | 796
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116 | 133
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4 4 4 | 45 |

ALIGNMENTS

| RESULT 1 D83506 conserved hypothetical protein PA1107 [imported] - Pseudomonas aeruginosa (strain PAO conserved hypothetical protein PA1107 [imported] - Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: D83506 R; Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. i. Lory, S.; Olbson, M.V. Nature 406, 959-964, 2000 A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A; Reference number: A82950; MUID: 20437337 A; Accession: D83506 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-398 <sto> A; Residues: 1-398 <sto> A; Cross-references: GB:AE004541; GB:AE004091; NID:g9947024; PIDN:AAG04496.1; GSPDB:GN C; Genetics: A; Gene: PA1107</sto></sto> |
|---|
|
Query Match 83.9%; Score 47; DB 2; Length 398; Best Local Similarity 30.4%; Pred. No. 52; Matches 7; Conservative 15; Mismatches 1; Indels 0; Gaps 0; Qy 1 SMSIARLGGXXXXXXXXXXXXXX 23 |
|
RESULT 2 S28059 serum response factor-related protein SL1 - African clawed frog C; Species: Xenopus laevis (African clawed frog) C; Species: Xenopus laevis (African clawed frog) C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000 C; Accession: S28059 R; Chambers, A.E.; Kotecha, S.; Towers, N.; Mohun, T.J. EMBO J. 11, 4981-4991, 1992 A; Title: Muscle-specific expression of SRF-related genes in the early embryo of Xenop A; Reference number: S28059; MUID:93099873 A; Recession: S28059 A; Molecule type: mRNA A; Residues: 1-498 CCHA> A; Residues: 1-498 CCHA> A; Cross-references: EMBL:219124; NID:965204; PIDN:CAA79531.1; PID:965205 C; Superfamily: serum response factor DNA-binding domain homology F; 2-57/Domain: serum response factor DNA-binding domain homology |
|
Query Match 82.1%; Score 46; DB 2; Length 498;
Best Local Similarity 27.3%; Pred. No. 1e+02;
Matches 6; Conservative 15; Mismatches 1; Indels 0; Gaps 0; |

Gaps

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A; Status: preliminary
A; Molecule type: DNA
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A; Residuas: 1-338 <SIN>
A; Residuas: 1-338 <SIN>
A; Cross-references: GB: AE003988; GB: AE003849; NID: 99106653; PIDN: AAF84419.1; GSPDB: GN
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinard, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000.
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chdo, M.A.; Madeira, A.M.B.N.; Madelara, H.M.F.; Mario, C.L.; Marques, M.V.; Martins
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., Wa.; de All.
A; Reference number: A59328
A; Reference number: A59328
A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: B82660
C;Accession: B82660
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable fructokinase F28G11.11 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: G96689
                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <BOC>
A;Cross-references: EMBL:X81461; NID:g608705; PIDN:CAA57218.1; PID:g608707
C;Superfamily: ribokinase
C;Reywords: phosphotransferase
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                                 submitted to the EMBL Data Library, September 1994 A; Reference number: S52160 A; Accession: S52161
                                                                                                                                                                                                                                                                                                                                                                        DB
91;
                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.4%; Score 45; DB Best Local Similarity 26.1%; Pred. No. 91; Matches 6; Conservative 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SMSIARLGGXXXXXXXXXXXX 23
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C; Accession: S52161
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R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Isture 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor A; Reference number: A82950; MUID:20437337
A; Accession: C83338
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004673; GB:AE004091; NID:g9948501; PIDN:AAG05842.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                            C; Accession: T47846
R; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, March 2000
A; Reference number: 224478
A; Accession: T47846
A; Status: preliminary
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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A;Introns: 504/3; 531/3; 575/3; 647/3; 679/2; 700/3; 759/2; 861/3
A;Note: T8B10.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.1%; Score 46; DB 2; Length 928; 26.1%; Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL138646
A;Experimental source: cultivar Columbia; BAC clone T8B10
C;Genetics:
                                                                                                                                                                                                                                     Arm repeat containing protein-like - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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C;Species: Escherichia coli
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16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               548 SMEVARAGGVHALVMLARNCKYE 570
                                                          292 MSVQRLGGVSQATHSLTTPVVS 313
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26.18;
                           2 MSIARLGGXXXXXXXXXXXX
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Best Local Similarity 26.1
Matches 6; Conservative
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Matches 6; Conserv
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C;Accession: J01419
R;Ueng, P.P.; Vincent, J.R.; Kawata, E.E.; Lei, C.H.; Lister, R.M.; Larkins, B.A.
J. Gen. Virol. 73, 487-492, 1992
A;Title: Nucleotide sequence analysis of the genomes of the MAV-PS1 and P-PAV isolate A;Reference number: J01409; MUID:92166764
A;Accession: J01419
                                                  R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
                                                                                                                                                                                 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A85595

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-402 <STO>

A;Cross-references: GB:AE005174; NID:g12513857; PIDN:AAG55221.1; GSPDB:GN00145; UWGP:

A;Experimental source: strain 0157:H7, substrain EDL933

C;Genetics:
A;Genetics:
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C.Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 20-Jun-2000
           16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: genomic RNA
A; Residues: 1-450 <MIL>
A; Cross-references: EMBL: X07653; NID:g58798; PIDN: CAA30495.1; PID:g1334818
A; Note: 422-11e was also found
C; Superfamily: potato leaf roll virus 80k protein; potato leaf roll virus c
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R;Miller, W.A.; Waterhouse, P.M.; Gerlach, W.L.
Nucleic Acids Res. 16, 6097-6111, 1988
A;Title: Sequence and organization of barley yellow dwarf virus genomic A;Reference number: S00946; MuID:88289355
A;Accession: S00950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical 49.8K protein - barley yellow dwarf virus (isolate P-PAV) N'Alternate names: ORF5 protein C;Species: barley yellow dwarf virus, BYDV C;Species: barley yellow dwarf virus, BYDV C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein, 50K - barley yellow dwarf virus (fragment)
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Pred. No. 1.2e+02;
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Pred. No. 1.4e+02;
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SISVSKLGGQSMQYIENEKCETK
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21.7%;
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26.1%;
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Best Local Similarity
Matches 5; Conserva
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Best Local S
Matches 6
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A; Accession: E64822
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-402 < BLAT>
A; Cross-references: GB:AE000186; GB:U00096; NID:91787058; PIDN:AAC73932.1; PID:91787068;
A; Cross-references: GB:AE000186; GB:U00096; NID:91787058; PIDN:AAC73932.1; PID:91787068;
A; Cross-references: GB:AE000186; GB:U00096; NID:91787058; PIDN:AAC73932.1; PID:91787068;
A; Experimental source: strain K-12, substrain MG1655
C; Superfamily: cynX protein
C; Keywords: transmembrane #status predicted <TM1>
F; 52 68/Domain: transmembrane #status predicted <TM4>
F; 79-95/Domain: transmembrane #status predicted <TM6>
F; 117-187/Domain: transmembrane #status predicted <TM6>
F; 117-187/Domain: transmembrane #status predicted <TM5>
F; 117-187/Domain: transmembrane #status predicted <TM7>
F; 342-35A/Domain: transmembrane #status predicted <TM7>
F; 342-35A/Domain: transmembrane #status predicted <TM7>
F; 342-35A/Domain: transmembrane #status predicted <TM7>
F; 369-385/Domain: transmembrane #status predicted <TM9>
F; 369-385/Domain: transmembrane #status p
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G96689
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C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: E64822
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A,; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
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1.2e+02;
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Best Local Similarity 26.14
Best Local 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-384 <STO>
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Matches 6; Conserv
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Gaps

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conserved hypothetical protein frameshift TC0408 [imported] - Chlamydia muridarum (st C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C; Accession: E81706
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A; Recence number: A81500; MUID:2015025
A; Accession: E81706
A; Status: preliminary
A; Residues: 1-826 < ATER>
A; Residues: 1-826 < ATER>
A; Cross-references: GB: AE002307; GB: AE002160; NID: 97190442; PIDN: AAR39264.1; PID: 9719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dypothetical protein D1044.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_reprised from GB/EMBL/DDBJ
A;Reference number: 218423
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Reference preliminary;
A;Rolecule type: DNA
A;Residues: 1-1895 FARDU-
A;Cross-references: EMBL:U00065; NID:9495681; PID:9495684; PIDN:AAA50735.1; CESP:D104
A;Experimental source: strain Bristol N2
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A;Gene: CESP:D1044.3
A;Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: strain Nigg (MoPn) C, Genetics:
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Job time: 141 sec
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83100
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337
A;Accession: F83100
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A Molecule type: DNA
A; Residues: 1-687 - SSTO>
A; Cross-references: GB:AE004852; GB:AE004091; NID:g9950587; PIDN:AAG07755.1; GSPDB:GN001
A; Experimental source: strain PAO1
A; Genetics:
A; Genetics:
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A;Introns: 49/1; 91/3; 139/2; 179/2; 221/2; 270/1; 311/3; 342/2; 399/1; 481/1; 510/2; E
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF067949; PIDN:AAC19238.1; GSPDB:GN00023; CESP:T10H9.5
A;Experimental source: strain Bristol N2; clone T10H9
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T33240
R;Greco, T.; Bradshaw, H.; O'Brien, D.
submitted to the RMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T10H9.
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      21.7%; Pred. No. 1.4e+02; ive 18; Mismatches 0;
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Pred. No. 1.9e+02;
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26.1%;
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      Best Local Similarity 21.7 Matches 5; Conservative
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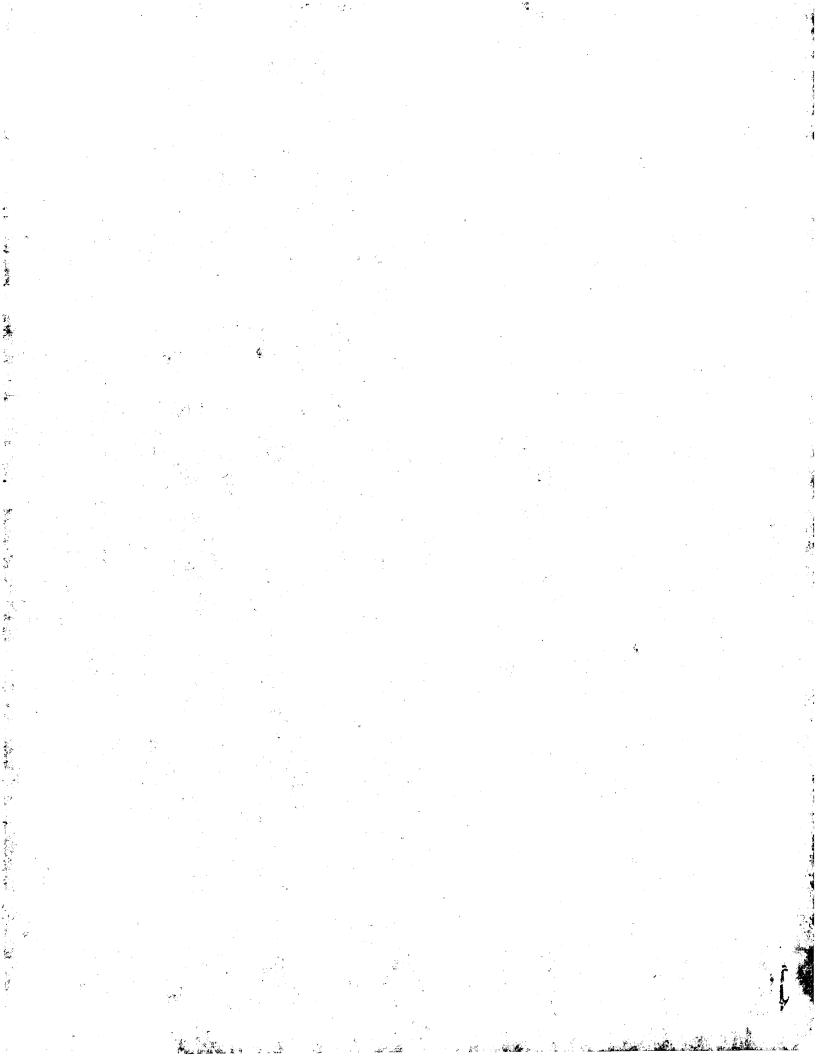
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4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-814-817-2
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US-08-180-371-2
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US-08-458-067-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                               - protein search, using sw model
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                                                                                                                                                                                                                                                                                       Title:
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       Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 8, A Sequence 8, A Sequence 1, A Sequence 1, A Sequence 3, A Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reznikoff, William S
APPLICANT: Gorysin, Igor Y
APPLICANT: Zhou, Hong
ITILE OF INVENTIONS: System for In Vitro Transposition
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/850,880 FILING DATE:
PCT-US96-07795-2
PCT-US96-07796-2
US-07-9306-595C-8
US-09-181-706-8
US-09-459-066-8
US-09-459-066-8
US-08-910-925-4
US-08-910-925-1
US-08-910-925-1
US-08-910-925-1
US-08-097-767A-38
US-07-603-133B-13
US-07-603-133B-15
US-08-813-940-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-466-390-4
US-08-470-950-4
US-08-467-781-4
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08850880 Patent No. 5925545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 9607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 MSIARLGGXXXXXXXXXXX 23
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Best Local Similarity 31.89
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-850-880-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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Gaps
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                             CALP: 33/03

COUNTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELADABLE FORM:
CORPUTER: Ploppy disk
CORPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,877
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 960296.94142

REGISTRATION NUMBER: 960296.94142

TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000

TELEPAC: 608/251-5000

TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: Allocation acids
TYPE: Allocation acids
TYPE: Allocation acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT:
Dasmahapatra, Bimalendu
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: One diraida Farms
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57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,901
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,988
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/509,007
FILING DATE: 10-APR-1990
APPLICATION NUMBER: 07/509,007
FILING DATE: 13-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: DULAK, NO. 5559906man C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.5%; Score 49;
31.8%; Pred. No.
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Patent No. 5599906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 31.8%
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-814-877-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Madison
STATE: New Jersey
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-333-901-2
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Sequence 2, Application US/08814877

Sequence 2, Application US/08814877

Fatent No. 5965443

GENERAL INFORMATION:
APPLICANT: Goryshin, Igor Y
APPLICANT: Reznikoff, William S

TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 476;
                                                  Sequence 2, Application US/08944916
Patent No. 5948622
GENERAL INFORMATION:
APPLICANT: Reznikoff, William S
APPLICANT: York, Dona L
APPLICANT: Zhou, Hong
TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.5%; Score 49; DB 2; 31.8%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/814,877
FILING DATE: 09-SEP-1996
PRIOR APPLICATION NUMBER: US 08/850,880
FILING DATE: 02-NAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEFAX: 608-251-9166
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 31.8*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                         CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 53703
                                US-08-944-916-2
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APPLICANT: Otack, Hideko
APPLICANT: Coyama, Yasuji
APPLICANT: Koyama, Yasuji
APPLICANT: Koyama, Yasuji
APPLICANT: Novama, Yasuji
APPLICANT: Novama, Yasuji
APPLICANT: Novama, Filchi
TITLE OF INVENTION: N-Acetylmannosamine Dehydrogenase Gene and
TITLE OF INVENTION: Productin of N-Acetylmannosamine Dehydrogenase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.8%; Score 43; DB 2; Lei
30.0%; Pred. No. 1.9e+02;
iive 14; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
                      Schering-Plough Corporation
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
ODFERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/898,789
FILING DATE: 23-JUL-1997
CLASSIFICATION OF TAX
APPLICATION NUMBER: 07/923,988
FILING DATE: 21-SEP-1992
APPLICATION NUMBER: 07/923,988
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/509,007
FILING DATE: 13-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: DULAK, NO. 5891635man C.
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/637,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/07637865
Patent No. 5942427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 IARLGGDEFTFKKLIRDSGQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 IARLGGXXXXXXXXXXXX 23
                                             One Giralda Farms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.0%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-898-789-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1990122
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
    CORRESPONDENCE ADDRESS:
                                                             Madison
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                  07940
                                                                                                               COUNTRY:
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                                                                                                                                                           Gaps
                                                                                                           Ouery Match 76.8%; Score 43; DB 1; Length 236; Best Local Similarity 30.0%; Pred. No. 1.9e+02; Matches 6; Conservative 14; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.8%; Score 43; DB 1; Length 236; 30.0%; Pred. No. 1.9e+02; tive 14; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dasmahapatra, Bimalendu
TITLE OF INVENTION: No. 5721133el Protease Assays
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: One Giralda Farms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-08-898-789-2
US-08-898-789-2
Sequence 2, Application US/08898789
Partent No. 5891635
GENERAL INFORMATION:
APPLICANT: Dasmahapatra, Bimalendu
TILLE OF INVENTION: No. 5891635el Protease Assays
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,582
FILING DATE: 01-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/923,988
FILING DATE: 21-SEP-1992
APPLICATION NUMBER: PCT/US91/02283
FILING DATE: 10-APR-1991
APPLICATION NUMBER: PCT/US91/02283
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/509,007
FILING DATE: 11-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: DULAK, NO: 5721133man C.
                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08456582 Patent No. 5721133
                                                                                                                                                                                                                           182 IARLGGDEFTFKKLIRDSGQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 IARLGGXXXXXXXXXXX 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
               ; MOLECULE TYPE: peptide US-08-333-901-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-456-582-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Madison
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 07940
                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-456-582-2
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Patent No. 6031154
GENERAL INFORMATION:
PAPPLICANT: Bennett, Alan B.
APPLICANT: Ranayama, Yoshinori
TITLE OF INVENTION: Pructokinase Genes and Their Use in
TITLE OF INVENTION: Metabolic Engineering of Fruit Sweetness NUMBER OF SEQUENCES: 6
CORRESPONDENCES ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3170;
                                                                                                                                                                                                                                           APPLICANT: Donadio, S
APPLICANT: Katz, L
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Polyketides
CORRESPONDENCES: 27
ADDRESSEE: Steven F. Weinstock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%; Score 42; DB 3; Length 317
26.1%; Pred. No. 1.6e+04;
Live 15; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Steven F. Weinstock .
STREET: Abbott Laboratories D377/AP6D-2 One Abbott STREET: Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  6; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .., VE
....ER: US/08/439,009A
NI: 435
TWY
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Patent No. 6004787
                                                                 668 SRVLARLGGQGGMASFGLGTEQA 690
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                                          1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 3170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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STATE: 1L
COUNTRY: US
TTO: 60064-3500
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11 CLASSIFICATION:
                                                                                                                                                                  US-08-439-009A-5
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      Matches
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APPLICANT: Ratz, L
APPLICANT: Donadio.
TITLE OF INVENTION: EFYTHCOMPOINT FOR TITLE OF INVENTION: EFYTHCOMPOINT OF SEQUENCES:
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3170;
                                                                                                                                                                                                                                                                                                                                                                         Length 271;
                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.8%; Score 43; DB 2; Length 271
Best Local Similarity 23.8%; Pred. No. 2.4e+02;
Matches 5; Conservative 16; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 2; Pred. No. 1.6e+04;
                                                          NAME: Skerpon, Joseph M.
REGIGSTRATION NUMBER: 29,864
REFERENCE/DOCKET NUMBER: 0118.03382
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-296-5500
TELEPHONE: 202-296-7830
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: JP 01-338267
FILING DATE: 28-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/07642734C Patent No. 5824513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DANCKETS, AND REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 495:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 708-937-9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 AVARLGGLDILVAGGALKGGT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SIARLGGXXXXXXXXXXX 23
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26.1%;
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TENGTH: 3170 amino acids
                                                                                                                                                                                                                            LENGTH: 271 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-07-637-865-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60064-3500
COMPUTER READABLE FORM:
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3Y: linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-642-734C-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-642-734C-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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Length 493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bortner, Scott R.
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: WEYR 20050 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tal, Ronny
APPLICANT: Benziman, Moshe
APPLICANT: Benziman, Moshe
APPLICANT: Gelfand, David H.
APPLICANT: Ben-Bassat, Arie
APPLICANT: Galhoon, Roger D.
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE
TITLE OF INVENTION: METABOLIC ENZYMES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

SOFTWARE: Patentin Release #1.0,

SOFTWARE: PATENTON NUMBER: PCT/US92/08756A

FILING DATE: 19921014

CLASSIFICATION DATA:

APPLICATION PATA:

APPLICATION PATA:

APPLICATION PATA:

APPLICATION PATA:

APPLICATION PATA:

APPLICATION PATA:

AND PATANTER PATATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application PC/TUS9208756A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2001 Ferry Building CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                               Acetobacter xylinum
                     TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERLETICS:
LENGTH: 493 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 AISRLGGDEFAIILRRSLKLM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SIARLGGXXXXXXXXXXX 23
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TELEX: 278356
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 493 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
PCT-US92-08756A-11
                                                                                                                                                                                                                                                                                           ORGANISM:
US-08-309-512-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC ENZYMES
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STAME: California
COUNTRY: U.S.A.
ZIP: 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.2%; Score 41; DB 3; Length 328; 17.4%; Pred. No. 7.1e+02; tive 18; Mismatches 1; Indels
                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/826,611

FILING DATE: 05-APR-1997

CLASSIFICATION NUMBER: US/08/826,611

FILING DATE: 34,774

REGISTRATION NUMBER: 34,774

REGISTRATION NUMBER: 023070-077400US

TELEPHONE: (415) 576-0300

TELEPHONE: (415) 576-0300

INFORMATION FOR SED ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 328 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,218
FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bortner, Scott R. REGISTRATION NUMBER: 34,298 REFERENCE/DOCKET NUMBER: 8145-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08309512
Patent No. 575828
GENERAL INFORMATION:
APPLICANT: Tal, Ronny
APPLICANT: Benziman, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 AIAVTRLGGKSAFVGKLGDDEFG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SMSIARLGGXXXXXXXXXXXX 23
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Benziman, Moshe
Gelfand, David H.
Ben-Bassat, Arie
Calhoon, Roger D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-826-611-6
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-08-309-512-11
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73.2%; Score 41; DB 5; Length 507; 23.8%; Pred. No. 1.4e+03;
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STOREY, Gerald A.
COUGHLIN, Richard T.
COUGHLIN. GHARACTERIZATION OF GRANULOCYTIC
EHRLICHIA AND METHODS OF USE
                                                                                                                 APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Cytochrome P450lpr Gene and Its
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFEAX: 716-263-1600
                                                                                                                                                                                                                     ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: P.O. Box 1051, Clinton Square CITY: Rochester STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                            Sequence 22, Application PC/TUS9505758 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHROMOSOME/SEGMENT: Chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 SISKLGGLTFNELAAQVFVFF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: Adult
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 507 amino acids TYPE: amino acid
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE
                                                          PCT-US95-05758-22
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                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
APPLICANT: Tomita. Takashi
TILE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Nechester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.2%; Score 41; DB 1; Length 507; 23.8%; Pred. No. 1.4e+03; Live 16; Mismatches 0; Indels
                                                                                                                                        73.2%; Score 41; DB 5; Length 493; 23.8%; Pred. No. 1.4e+03; Live 16; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,274A
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                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08457274A Patent No. 5734086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 800
ATTORNEYAGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEDRIONE: 716-263-1304
TELEFRAX: 716-263-1600
                ANTI-SENSE: NO
ORIGINAL SOURCE:
CRGANISM: Acetobacter xylinum
PCT-US92-08756A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 507 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 SISKLGGLTFNELAAQVFVFF 303
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DEVELOPMENTAL STAGE: Adult
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ORGANISM: Musca domestica
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Best Local Similarity 23.8%
Matches 5; Conservative
                                                                                                                                        Query Match 73.28
Best Local Similarity 23.88
Matches 5; Conservative
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COMPUTER READABLE FORM:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-457-274A-22
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Search completed: May 8, 2002, 07:29:16 Job time: 74 sec

242 SFESARLGGLSVGFSYSPTGYRD 264

1 SMSIARLGGXXXXXXXXXXXX 23

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May 8, 2002, 07:28:02 ; Search time 38.64 Seconds (without alignments) 44.091 Million cell updates/sec
GenCore version 4.5 . Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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56
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Run on:

Title:

Total number of hits satisfying chosen parameters:

522463 seqs, 74073290 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_1101:* Database :

/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | Prostate homing an | Chimeric prostate- | pJDB-neo-ATE trans | Modified (transpos | Mutant In5 transpo | Wildtype In5 trans | Mutant In5 transpo | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SUMMARIES | ID Salmer Ass | AAB21938 | AAE06513~ | . AAR07414 | AAW56694 | AAY42535 | AAY42536 | AAY42537 | AAY42538 | AAY42539 | AAY42540 | AAY42541 |
| | Query
Match Length DB_ID | 23 21 | 23_22 | 49 11 | 476 19 | 476 20 | 476 20 | • | • | 476 20 | • | • |
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| | Result
No. Score | 1 | ₹'
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WPI; 2000-499174/44.

| Mutant Tn5 transpo
Mutant Tn5 transpo
Mutant Tn5 transpo
Modified Tn5 trans
Wild-type Tn5 tran
Bucalyptus grandis | protein
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protein | nterococcus
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AAY15382
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AAG9235
AAB7888
AAY8249 | AAY0021
AAY0021
AAM2202
AAM3839
AAB2530
AAB2530 | | AAW47125
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AAW58897
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23 | 0 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 |

ALIGNMENTS

Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human. Pasqualini R, Ruoslahti EI; Prostate homing antimicrobial pro-apoptotic conjugate. Key Location/Qualifiers Misc-difference 10..23 /note= "Preferably D-form residues" AAB21938 standard; Peptide; 23 AA. 99US-0235902. 21-JAN-2000; 2000WO-US01602. 22-MAR-2001 (first entry) Ellerby HM, Bredesen DE, Chimeric - Homo sapiens. Chimeric - Unidentified. (BURN-) BURNHAM INST. WO200042973-A2 22-JAN-1999; 27-JUL-2000. AAB21938; AAB21938 RESULT

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RESULT
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                                                                                 comprising of a tumour homing molecule that selectively homes to a mammaalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammaalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such prostate homing pro-apoptotic conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
        Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
                                                                       The present invention relates to homing pro-apoptotic conjugates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ellerby HM;
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                                                                                                                                                                                                                                   DB 21; Length 23;
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/note= "Glycinylglycine bridge"
10..23
/label= Antimicrobial_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric prostate-homing pro-apoptotic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Prostate_homing_domain
                                                                                                                                                                                                                        100.0%; Score 56; DB Z
                                                                                                                                                                                                                                                       14; Mismatches
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                                                  Claim 29; Page 108; 118pp; English
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                                                                                                                                                                                                                                                                                                                                                    AAE06513 standard; peptide; 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-2000; 2000US-0489582
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic.
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                   Query Match
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Matches
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                                              The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vector for detection of regulatory sequence - by using combination of plasmids with different expression powers etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 23;
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31.8%; Pred. No. 5.6;
Live 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                                                                                              prostate-homing pro-apoptotic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pJDB-neo-ATE translation product 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä.
Claim 6; Page 103; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMSIARLGGXXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR07414
ID AAR07414 standard; protein; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter; Neo structural gene.
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Best Local Similarity 31.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-315505/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TOFU ) TONEN CORP
                                                                                                                                                                                                                                                                                                                                                                   23 AA;
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                                                                                                                                                                                                                                                                                                                                                                      Sequence
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AAY42535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified Tn5 transposase construct used in novel system for in vitro transposition - used to, e.g. create absolute defective mutants, provide selective markers and to facilitate insertion of specialised DNA sequences into target DNA
                                                                                                                                                                                                                                                                                             Tn5 transposase; modified; enzyme; in vitro transposition; mutant;
target; marker; transposon 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                /label- E54K
/note- "wild type Glu is replaced by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "wild type Leu is replaced by Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "wild type Met replaced by Ala"
                                                                                                                                                                                                                                                            Modified (transposon 5) In5 transposase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Pages 31-33; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                            AAW56694 standard; Protein; 476 AA.
                                     2 MSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= L372P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= M56A
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96US-0814877
                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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09-SEP-1996;
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                                                                                                                                                                                AAW56694;
                                               56
                                                                                                                           AAW56694
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This sequence represents mutant Tn5 transposase EK54 MA56 LP372. This mutant form differs from the wildtype in that it binds to repeat sequences of donor DNA with greater avoidity than the wildtype Tn5 transposase and it is less likely than the wildtype protein to assume an inactive multimeric structure. The improved avidity of the modified transposase for the Oreside End (DE) terminic is due to the Lys residue at amino acid 54, which is Glu in wild type Tn5 transposase (AAV42536). The mutation strongly alters the preference Tof the Iransposase (AAV42536). The mutation, known as EK54, to OE termini. The higher binding of this mutation, known as EK54, to OE termini results in a transposase. Similar changes at position 54 to the name and position 47 (Thr to Pro change) also result in increased binding to the OE termini. The reduction in the formation of the inactive mutimeric form is achieved by modifying amino acid 372 (Leu) of wildtype Tof Transposase to Pro (LP372). This sequence also has a substitution of Than for miditype Met at position 56. This substitution prevents the translation of an inhibitor protein, the initiation creased.
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than can be achieved using wild type transposase (as measure in vivo). In vitro transposition using this system can also use donor DNA and target DNA that is circular or linear. The system also requires no outside high energy source and no other protein other than the modified
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                                                                                                                                                                                                                                                                                                                    87.5%; Score 49; DB 19; Length 476; 31.8%; Pred. No. 1.4e+02; Live 15; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant Tn5 transposase EK54 MA56 LP372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY42535 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MSIARLGGXXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0814877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ22881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-1996;
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                                                                                                                                                  ransposase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY42535;
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                                                                                                                                                 transposase enzyme is useful in a system for introducing genetic changes to nucleic acid. The method can be applied to create absolute defective mutants, to provide selective markers to target DNA, to provide portable regions of homology to a target DNA, to facilitate insertion of specialised DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequencing, and to facilitate production of genetic fusions for gene expression studies and protein domain mapping.
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corresponds to the sequence encoding wildtype Met 56. As a result, the mutant transposase exhibits a somewhat higher transposition rate. The Tn5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to Mu- and Tn10-based systems. The mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.5%; Score 49; DB 20; Length 476; 31.8%; Pred. No. 1.4e+02;
Live 15; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 maiarlggfmdskrtgiaswga 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 MSIARLGGXXXXXXXXXXX 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  changes to nucleic acid
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               476 AA;
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char42538, AAY42540) and position 47 (Thr to Pro change, TP47, AAY42542))

also result in increased binding to the OE termini. Mutants with a also result in increased binding to the OE termini. Mutants with a substitution of Ala for wildtype Met at position 5 exhibited a higher transposition rate than the wildtype. This substitution prevents the transposition rate than the wildtype. This substitution prevents the carnal action of an inhibitor protein, the initiation codon of which corresponds to the sequence encoding wildtype Met 56. The TR5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to Mu- and Th10-based systems. The mutant transposase enzyme is useful in a system for introducing genetic changes to nucleic actid. The method can be applied to create absolute defective mutants, to provide selective markers to target DNA, to provide primer binding sites or tags for DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequences categorical statics and protein domain mapping.

Note: The present sequence is not shown in the specification but is derived from the mutant Tn5 transposase sequence given in columns 15-18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified transposase enzyme for use in a system for introducing genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transposase; modified form; wildtype; mutant; multimeric; OE termini; IE termini; outside end termini; inside end termini; repeat sequence; mutation; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 476;
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31.8%; Pred. No. 1.4e+02;
iive 15; Mismatches 0;
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Best Local Similarity 31.8%
Matches 7; Conservative
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is due to the Lys residue at amino acid 54, which is Glu in wild type Transposase (AAV12536). The mutation strongly alters the preference of the transposase (Dr. the OB termini, as opposed to the Inside End (IE) termini. The higher binding of this mutation, known as EK54, to OE termini. The higher binding of this mutation, known as EK54, to OE termini results in a transposaic. The reduction in the formation of the inactive multimeric form is achieved by modifying amino acid 372 (Leu) of wildtype Tn5 transposase to Pro (LP372). The Tn5-based transposation system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to Mu- and Tn10-based systems. The modified transposase enzyme setul in a system for introducing genetic changes to nucleic acid. The method can be applied to create absolute defective mutants, to provide selective markers to target DNA, to provide portable regions of homology to a target DNA, to provide primer binding sites or tags for DNA sequencing, and to facilitate production of genetic fusions for gene where the produce of the provide selective markers contained production of genetic fusions for gene where the produce of the provide selective markers of acilitate production of genetic fusions for gene where the produce of the provide production of genetic fusions for gene where the production of genetic fusions for gene where the production of genetic fusions for gene where the production of provide selective markers and protein domain mapping.
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31.8%; Pred. No. 1.4e+02;
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Matches 7; Conservative
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Synthetic.
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Transposace for the repeat sequences for the Outside End (OE) termini is due to the Val residue at amino acid 54, which is Glu in wild type is due to the Val residue at amino acid 54, which is Glu in wild type fransposace (AAV4236). The mutation strongly alters the preference of the transposace for the OE termini, as opposed to the Inside End (IE) termini results in a transposace. The reduction in the formation of the cermini results in a transposace. The reduction in the formation of the inactive multimeric form is achieved by modifying amino acid 372 (Leu) of wildtype Tr5 transposace to Pro (L972). The Tr5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to Mu- and Tull-based systems. The modified transposace enzyme is useful in a system for introducing genetic changes to nuclaic acid. The method can be applied to create absolute defective mutants, to provide selective marget DNA, to facilitate insertion of specialised DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequencing, and to facilitate production of genetic fusions for gene expression studies and productin domain mapping.
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inactive multimeric structure. The improved avidity of the modified
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Best Local Similarity 31.85
Matches 7; Conservative
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seen with wild-type transposase. The In5-based transposition
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          transposase. The improved avoidity of the modified transposase. The improved avoidity of the modified transposase for the repeat sequences for the Outside End (OE) terminist due to the Lys residue at amino acid 54, which is Glu in wild type Tn5 transposase (AA42536). The mutation strongly alters the preference of the transposase for the OE termini, as opposed to the Inside End (IE) termini. The higher binding of this mutation, known as EK54, to OE termini. The higher binding of this mutation, known as EK54, to OE termini. The higher transposition rate that is about 10-fold higher than seen with wild-type transposase. The Tn5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to
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 sequences of donor DNA with greater avidity than the wildtype Tn5
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15; Mismatches 0; Indels
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                                                                                                                                                                                                                                                            87.5%;
31.8%;
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system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared Mu- and Tn10-based systems.
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY42541 standard; protein; 476 AA.
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                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                             2 MSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                 87.5%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant In5 transposase LP372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0814877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goryshin IY;
                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-579916/49.
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                                                                                                                                                                  476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transposon In5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reznikoff WS,
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AAY42542;

AAY42542

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AAY42543 standard; Protein; 476 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 MSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WISC ) WISCONSIN ALUMNI RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0814877.
                                                                                                                                                     Mutant In5 transposase MA56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0814877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goryshin IY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 31.8<sup>†</sup>
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       changes to nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-579916/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476 AA;
                                                                                                                                                                                                                                                                                                             Transposon In5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reznikoff WS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-1996;
                                                                                                  20-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                     US5965443-A
                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY42544;
                                                  AAY42543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY42544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents mutant Tn5 transposase TP47. This mutant form differs from the wildtype in that it binds to repeat sequences of donor DNA with greater avidity than the wildtype Tn5 transposase. The improved avidity of the modified transposase or the repeat sequences for the Outside End (OE) terminity of the modified transposase for the repeat sequences for the Outside End (OE) terminity of the pro residue at maino acid 47, which is Thr in wild type of the transposase (AAV4536). The mutation strongly alters the preference of the transposase for the Outside End (IE) terminity The higher binding of this mutation, known as TP47, to OE terminity results in a transposition rate that is about 10-fold higher than seen with wild-type transposase. The Tn5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to will apply that are active on DNA of any structure when compared to the transposition that are active on DNA of any structure when compared to will apply that the transposition that are active on DNA of any structure when compared to the transposition that are active on DNA of any structure when compared to the transposition that the transposition that the acid th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified transposase enzyme for use in a system for introducing genetic
                                                                                                                                                                                                                                                                                                                                                                                                          Transposase; modified form; wildtype; mutant; multimeric; OE termini; IE termini; outside end termini; inside end termini; repeat sequence; mutation; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.5%; Score 49; DB 20; Length 47 31.8%; Pred. No. 1.48+02; ive 15; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                  AAY42542 standard; protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page -; 21pp; English.
                                                  2 MSIARLGGXXXXXXXXXXX 23
                       2 MSIARLGGXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0814877
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                                                                                                                                                                                                                                                                                                                                                          Mutant In5 transposase TP47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reznikoff WS, Goryshin IY;
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 87.5
Best Local Similarity 31.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transposon In5.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-1996;
                                                                                                                                                                                                                                                                                                       20-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS5965443-A
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This sequence represents mutant Tn5 transposase MA56. This sequence has a substitution of Ala for wildtype Met at position 56. This substitution prevents the translation of an inhibitor protein, the initiation codon of which corresponds to the sequence encoding wildtype Met 56. As a result, the mutant transposase exhibits a somewhat higher transposition rate. The Tn5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that active on DNA of any structure when compared to Mu- and Tn10-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The present sequence is not shown in the specification but is derived from the mutant Tn5 transposase sequence given in columns 15-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified transposase enzyme for use in a system for introducing genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Transposase; modified form; wildtype; multimeric; OE termini; IE termini; outside end termini; inside end termini; repeat sequence; mutation; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transposase; modified form; wildtype; multimeric; OE termini; IE termini; outside end termini; inside end termini; repeat sequence; mutation; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.5%; Score 49; DB 20; Length 476; 31.8%; Pred. No. 1.4e+02; ive 15; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY42544 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page -; 21pp; English.
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Sequence

RESULT 13

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Search completed: May
             07-SEP-1999
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  δλ
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                                                                                                                                                                                                                                                             This sequence represents mutant Tn5 transposase EK54 MA56. This mutant form differs from the wildtype in that it binds to repeat sequences of donor DNA with greater avoidity than the wildtype Tn5 transposase and it is less likely than the wildtype protein to assume an inactive multimeric structure. The improved avoidity of the modified transposase for the routside End (DE) terminic is due to the Lys residue at amino acid 54, which is Glu in wild type Tn5 transposase (AAY42536). The mutation strongly alters the preference CC of the transposase for the Ose terminic The higher binding of this mutation, known as EK54, to OBE terminic The higher binding of this mutation, known as EK54, to OBE terminic results in a transposition rate that is about 10-fold higher compared to the negative prevents the translation of an inhibitor protein, the initiation codon of prevents the translation of an inhibitor protein, the initiation codon of the mutant transposase exhibits a somewhat higher transposition rate. The Tn5-based transposition system is more broadly applicable and cullises shorter, more well defined terminic that are active on DNA of any structure when compared to Mu- and Tn10-based systems.

CC derived from the mutant Tn5 transposase sequence given in columns 15-18.
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                                                                                                                                                                                                    Modified transposase enzyme for use in a system for introducing genetic changes to nucleic acid \dot{\mathbf{c}}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transposase; modified form; wildtype; multimeric; OE termini; IE termini; outside end termini; inside end termini; repeat sequence; mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 49; DB 20; Length 476; Pred. No. 1.4e+02; 15; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified In5 transposase enzyme amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY15382 standard; Protein; 476 AA.
                                                                                                                            (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                            Disclosure; Page -; 21pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.5%;
                                                                         96US-0814877
                                                                                                    96US-0814877
                                                                                                                                                     Reznikoff WS, Goryshin IY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity 31.0v
                                                                                                                                                                              WPI; 1999-579916/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 AA;
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                                                                         09-SEP-1996;
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                       US5965443-A.
                                                  12-OCT-1999
Synthetic.
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This is the amino acid sequence containing the modified form of the Transposase enzyme. This modified form differs from the wildtype in that the index to the repeat sequences of the donor DNA with greater avidity than the wildtype Tn5 transposase and it is less likely than the wildtype Tn5 transposase and it is less likely than the wildtype protein to assume an inactive multimeric structure.

The improved avidity of the modified transposase for the repeat caquences for the Outside End (OE) termini (class (1) mutation) can be achieved by providing a lysine residue at amino acid 54, which is glutamic acid in wild type Tn5 transposase. The mutation, known as EK54, to OE termini. The higher binding of this mutation, known as EK54, to OE termini results in a transposase. Similar changes at position 54 to valine and position 47 (threonine-to-proline change) also result in increase binding to the OE termini.

The reduction in the formation of the inactive multimeric form is achieved by modifying amino acid 372 (leucine) of wildtype Tn5 transposase to a proline (class (2) mutation, LP372).

The Th5-based transposition system is more broadly applicable and this increase shorter more well defined remaining that are acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNA of any structure when compared to Mu- and Tn10-based systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        defined termini that are active on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                     In vitro transposition using a In5 based genetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.5%; Score 49; DB 20; L
31.8%; Pred. No. 1.4e+02;
ive 15; Mismatches 0;
                                                                                                                                                                                                                                                                  Goryshin IY, Reznikoff WS, York DL, Zhou H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Column 27-31; 48pp; English.
                                                                                                                                                                                                    (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 maiarlggfmdskrtgiaswga 448
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97US-0944916.
                                                              97US-0944916.
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                                                                                                                               97US-0850880
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Best Local Similarity 31.07
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                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ06433
06-OCT-1997;
                                                              06-OCT-1997;
                                                                                                                               02-MAY-1997;
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OM protein - protein search, using sw model

May 8, 2002, 07:18:34; Search time 38.66 Seconds Run on:

(without alignments)
13.412 Million cell updates/sec

us-69-765-086-207 30 1 SMSIARL 7 Perfect score: Sequence:

BLOSUM62 Scoring table:

522463 seqs, 74073290 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_1101:*

| SIDS#Jgcgdata/geneseq/geneseqp/AA1980.DAT:*
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| SIDS#Jgcgdata/geneseqfyeneseqp/AA1988.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT.* /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT.* /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:

AAY48905

RESULT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | Membrane dipeptida | Human prostate-hom | Mouse prostate hom | Prostate homing an | Chimeric prostate- | C glutamicum prote | Arabidopsis thalia | C glutamicum prote | Protein involved i | Human novel protei | Human ORFX ORF1624 |
|---|-----------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| | ΠD | AAY48905 | AAB21907 | AAE06483 | AAB21938 | AAE06513 | AAGGUSB3 | AAG08955 | AAG91999 | AAY37469 | AAU14179 | AAB41860 |
| | ВО | 20 | 21 | 22 | 21 | 22 1 | 22 | 21 | 22 | 20 | 22 | 21 |
| | Query
Match Length DB ID | 7 | 7 | 7 | 23 | 23 | 236 | 191 | 289 | 301 | 183 | 260 |
| * | Query
Match | 30 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 1 | 90.0 | 0.06 | 0.06 | 86.7 | 86.7 |
| | Score | 30 | 30 | 30 | 30 | 30 | 29 | 27 | 27 | 27 | 26 | 56 |
| | Result
No. | н | 7 | 3 | 4 | 5 | ٥ | 7 | 80 | 6 | 10 | 11 |

| C glutamicum prote | Corynebacterium gl | ы | Eucalyptus grandis | Q, | Escherichia coli p | | E. coli growth and | Neisseria gonorrhe | C glutamicum prote | Human secreted pro | Human protein sequ | H. pylori cytoplas | H. pylori GHPO 153 | | | is | ω | is | ß | O | | Arabidopsis thalia | Rat calcitonin rec | Rat calcitonin rec | Protein encoded by | Human secreted pro | pJDB-neo-ATE trans | ¥ | | sts | #130 | Peptide #1337 enco | Peptide #1280 enco |
|--------------------|--------------------|---------|--------------------|-------------|--------------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----|----|----|----|---------|----|----|----|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------|------------|-----|------|--------------------|--------------------|
| | AAB7926 | AAW1803 | | 2 AAM4 0225 | | 2 AAG98916 | | | 3 AAG92942 | | | | | | | | | AAG0486 | | | | AAG21934 | | | AAB07564 | | | AAB4433 | L AAG55635 | | | AAM2730 | 2 AAM02598 |
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| 56 | 56 | 56 | 56 | 56 | 25 | 25 | 25 | 25 | 25 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 23 | 23 | 23 | 23 | 23 | 23 | 23 | 23 |
| 12 | 13 | 14 | 15 | 16 | 17 | 18 | . 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase. Membrane dipeptidase-binding prostate homing peptide #21. AAY48905 standard; Peptide; 7 AA. (first entry) Homo-sapeens. 10-DEC-1999 Synthetic. AAY48905;

W09946284-A2 6-SEP-1999 99WO-US05284 98US-0042107. 10-MAR-1999; 13-MAR-1998; 26-FEB-1999;

Ruoslahti EI; Pasqualini R, Rajotte D,

(BURN-) BURNHAM INST

WPI; 1999-571717/48.

New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological

Length 7;

7 AA;

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Sequence
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                                                                                                Matches
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                                                                  The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and Iymph node. The peptide bind to the membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; Page 107; 118pp; English.
                                    Claim 1; Page 151; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB21907 standard; Peptide; 7 AA.
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Best Local Similarity 100.v.
7; Conservative
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conditions
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; chimeric prostate-homing pro-apoptotic peptide;
prostate-homing peptide; antimicrobial peptide; prostate cancer;
tumour homing molecule; cytostatic.
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100.0%; Score 30; DB 22;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0;
  Score 30; DB 21;
Pred. No. 4.3e+05;
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ID AAE06483 standard; peptide; 7 AA.
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100.0%;
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Best Local Similarity
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                                                              cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
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                                                                                                                                                                       Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.
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                                                                                                                                        Prostate homing antimicrobial pro-apoptotic conjugate.
                                                                                                                                                                                                                                                                                                                 Key Location/Qualifiers
Misc-difference 10..23
/note= "Preferably D-form residues"
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                  AAB21938 standard; Peptide; 23 AA.
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Best Local Similarity 100.
Matches 7; Conservative
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Chimeric - Unidentified
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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                           /label= Coupling_domain
/note= "Glyciny1glycine bridge"
10.23
/label= Antimicrobial_peptide
                                                                                                                                                                                                                                    'label= Prostate_homing_domain
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                                                                                                                                                                                   Location/Qualifiers
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Matches 7; Conservative
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antimicrobial peptide -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-451901/48.
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99US-0128234.
99US-0128714.
99US-0129845.
99US-0130077.
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99US-0134219
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                                                                             99US-0126264
99US-0126785
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09-JUL-1999;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                          Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; SEQ ID NO: 4337; 246pp + Sequence Listing; English.
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                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                            07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                             18-DEC-2000; 2000EP-0127688
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Best Local Similarity 85.7
Matches 6; Conservative
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N-PSDB; AAH65802.
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2 smsvarl 8
                                                                                                             .6-DEC-1999;
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             EP1108790-A2.
                                                                                                                                                                                                          Nakagawa S,
Tateishi N,
                                           20-JUN-2001.
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RR 113-UL-1999) 9908-0142977,
RR 113-UL-1999) 9908-0142977,
RR 113-UL-1999) 9908-0142872,
RR 115-UL-1999) 9908-014282,
RR 115-UL-1999) 9908-0144321,
RR 115-UL-1999) 9908-0144331,
RR 12-UL-1999) 9908-0144331,
RR 12-UL-1999) 9908-0144331,
RR 12-UL-1999) 9908-0144332,
RR 12-UL-1999) 9908-0144333,
RR 12-UL-1999) 9908-0144334,
RR 12-UL-1999) 9908-0144333,
RR 12-UL-1999) 9908-0144334,
RR 12-UL-19
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG91999 standard; Protein; 289 AA
            990S-0157117.
990S-0157753.
990S-0157865.
990S-0158029.
990S-0158339.
990S-0158339.
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990S-0159329
990S-0159330
990S-0159331
990S-0159331
990S-0159638
990S-0159638
990S-0160741
990S-0160767
990S-0160814
990S-0160814
990S-0160814
990S-0160814
990S-0160819
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990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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85.7%;
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99US-0161406.
99US-0161359.
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 85.7
Matches 6; Conservative
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|12 smaiarl 18
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29 - SEP - 1999
04 - 0CT - 1999
05 - 0CT - 1999
07 - 0CT - 1999
13 - 0CT - 1999
13 - 0CT - 1999
14 - 0CT - 1999
14 - 0CT - 1999
14 - 0CT - 1999
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17 - 0CT - 1999
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18 - 0CT - 1999
21 - 0CT - 1999
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21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
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28-OCT-1999;
29-OCT-1999;
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26-OCT-1999;
28-OCT-1999;
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AAG91999
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                                                                                                                                                                                                       sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived
                                                                                                                                                                                                                                                                    from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, uncleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                              mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                              polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                          The present invention provides a number of nucleotide and protein
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                                                                                                                                                         Claim 17; SEQ ID NO: 5753; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein involved in intermediate metabolism of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 289;
50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY37469 standard; Protein; 301 AA.
 Ikeda M,
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85.7%;
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97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   European Patent Office
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Senoh A,
                               WPI; 2001-376931/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                289 AA;
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142 smsiarv 148
                                             N-PSDB; AAH67218
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17-DEC-1997;
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 Tateishi N,
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                                                                              Novel
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                             AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genttal diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibocterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides can be used to the polypeptides are used to identify compounds which bind to the
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
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                                                                                                                                                                                                                                                                                                           Length 301;
                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                             20;
Disclosure; Page 1157-1158; 1755pp; English.
                                                                                                                                                                                                                                                                                                           Score 27; DB;
Pred. No. 52;
1; Mismatches
                                                                                                                                                                                                                                                                                                             DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 555; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU14179 standard; Protein; 183 AA
                                                                                                                                                                                                                                                                                                             90.0%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human novel protein #50.
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
The 6; Conservē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-451939/48.
                                                                                                                                                                                                                                                        301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                      ||:||||
| 158 smaiarl 164
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                                                                                                                                                                                                                                                                                                                                                                                  1 SMSIARL 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2001
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                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU14179;
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polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine dual activity, to raise antibodies/elloit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating purns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthitis, anaemia, alzheimer's Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, arti-inflammatory diseases, nervous system disorders, and infection.

The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antitival; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malarta, autofimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 22; Length 183;
Pred. No. 55;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORFX ORF1624 polypeptide sequence SEQ ID NO:3248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB41860 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.78;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0127607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2000; 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.7
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SMSIARL 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1999;
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05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; heaptorcopic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimilant; cardiant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; and note of or preventing or treating pathological conditions and nucleic acids may be used to treat cancers; proliferative disorders, neurodegenerative disorders, osteoarthritis, collection, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic caneemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                   Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 21; Length 260;
Pred. No. 80;
2; Mismatches 0; Indels
                                                                      useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C glutamicum protein fragment SEQ ID NO: 5949.
                                                                                                                            Claim 11; Page 2449-2450; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG92195 standard; Protein; 382 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.78;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71...
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organic acid synthesis.
WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 AA;
                 N-PSDB; AAC76069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 smslari 214
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Tateishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
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                                                                                                                        The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                            ö
                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; monproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                   Claim 17; SEQ ID NO: 5949; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum SMP protein sequence SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 26; DB 22; Length 382; 71.4%; Pred. No. 1.2e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB79265 standard; Protein; 382 AA.
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99DE-1031413.
99DE-1031419.
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99DE-1031424.
99DE-1031428.
99DE-1031431.
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99DE-1031434.
99DE-1031510.
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                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                    European Patent Office.
 WPI; 2001-376931/40
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   :||:|||
192 amsvarl 198
            N-PSDB; AAH67414
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                                                                                                                                                                                                                                                                                                                                                                                                     1 SMSIARL 7
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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metabolism and oxidative phosphorylation (SMP) proteins given in metabolism and oxidative phosphorylation (SMP) proteins given in metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corprebacterium diphtheriae in a subject. (I), (II), (II) or host cells containing them are used to map genomes of organisms related to nevolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haberhauer G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schroeder H, Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 207-208; 1246pp; English.
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                                                                                                                                                99DE-1042076.
99DE-1042079.
99DE-1042086.
                            99DE-1032973
                                                             99DE-1033005
                                                                                         99DE-1040765
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99DE-1032924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pompejus M, Kroeger B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-061975/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AG.
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192 amsvarl 198
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                                                                                      27 - AUG - 1999
                                                                                                                                                                                                                    03-SEP-1999
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03-SEP-1999
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(first entry)

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Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals -
                                                                                                            Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistence; nutrient metabolism.
                                                                          Eucalyptus grandis cell signalling involved protein SEQ ID NO:940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 518-519; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Strabala TJ, Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                                                11-JAN-2000; 2000WO-US00724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-476052/41.
                                                                                                                                                                                                       Eucalyptus grandis.
                                                                                                                                                                                                                                          WO200042171-A1.
                                                                                                                                                                                                                                                                                                                                                      12-JAN-1999;
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                                       27-NOV-2000
                                                                                                                                                                                                                                                                              20-JUL-2000
   AAB25565;
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     Isolated retinoid X receptor protein - having amino acid insert in ligand binding domain, useful to identify specific target genes implicated in retinoid responses important in disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel retinoid X receptors RXR delta (AAW18032) and RXR epsilon (AAW18033) exhibit a high degree of amino acid conservation with other vertebrate RXRs but represent unique subtypes defined by an additional 14-amino acid segment in their ligand binding domains. These RXRs do not bind 9-cis retinoic acid (RA) or all-trans RA with high affinity and are not activated by 9-cis RA. They are able to form dimers in a manner equivalent to other RXRs. Their amino acid sequences were deduced from cDNA clones (AAMF67196-97) obtd. from adult and post-somitogenesis zebrafish cDNA libraries. The RXRs can be used to identify ligands, isolate mammalian counterparts, modify retinoid activity and identify target genes implicated in retinoid responses important in disease states.
                                                                                                                                                                                                                                                                          /note= "hinge between DNA-binding and ligand-binding domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.7%; Score 26; DB 18; Length 422; 71.4%; Pred. No. 1.4e+02; 1ve 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 /label- E
/note= "ligand-binding domain"
296..309
                                                                                                                                                                                                                                                                                                                                                                                       /note= "14-amino acid insert"
                                                                                                                                                                                                    /label= C
/note= "DNA-binding domain"
                                                                                                                                 1..89
/label= A/B
/note= "N-terminal domain"
90..156
                                      Retinoid X receptor; RXR delta; zebrafish
Zebrafish retinoid X receptor RXR delta.
                                                                                                              Location/Qualifiers
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Best Local Similarity 71.4*
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                                                                                                                                                                                                                                                                                                                  . 422
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                                                                          Brachydanio rerio.
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Domain
                                                                                                                                                                                    Domain
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99US-0228986. 99US-0162866.

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AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Bucalyptus grandis) or pine (Phnus radiata also known as Wonterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism: Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance considerations can be used to delay senescence of Ireproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between harvest and consumption, or to decrease branching frequency ir forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers.
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Pred. No. 2.3e+02;
2; Mismatches 0; Indels
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Similarity 71.4%;
5; Conservative ;
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Best Local Similarity
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92 slsvarl 98
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AAB25565 standard; Protein; 697 AA.

RESULT 15 AAB25565

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
PCT-US94-12550-48
PCT-US96-10041-26
US-08-723-306-23
PCT-US96-10041-23
US-07-908-455A-4
US-08-434-120-30
US-08-434-120-90
US-08-434-120-90
US-08-457-25-88
US-08-231-730A-24
US-08-457-798-24
US-08-457-171-24
US-08-457-171-24
US-08-457-171-24
US-08-457-171-24
US-08-457-171-24
US-08-505-486-24
US-08-505-486-24
US-08-505-486-24
US-08-505-486-24
US-08-505-486-24
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APPLICANT: MCLOUGHLID, MARK L
APPLICANT: BECKER, Callvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESSE: John H. Runnels
STREET: P. O. Box 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/232,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6. Application US/08944133
Patent No. 5789542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/POCKET NUMBER: Att;
TELECOMMUNICATION INFORMATION:
TELECHONE: 504 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Baton Rouge
STATE: LA
COUNTRY: USA
2IP: 70821-2471
COMPUTER READABLE FORM:
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LENGTH: 14 amino acids
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        STRANDEDNESS:
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US-08-944-133-6
        Query Match
        (without alignments)
15.190 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2444400,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                                                             Compugen Ltd
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US-08-231-730A-40
US-08-57-171-40
US-08-689-486-45
US-08-801-028-45
US-09-340-154-45
US-09-340-154-45
US-09-323-802A-40
PCT-US95-04335-40
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US-08-944-133-4
US-08-944-133-8
US-08-944-133-27
US-08-944-133-25
US-08-723-306-27
US-08-723-306-27
US-08-723-306-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-09338-45
PCT-US95-09339-45
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                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212252 segs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM protein – protein search, using sw model
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Maximum DB seq length: 200000000
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Match
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Sequence:
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TITLE OF INVENTION: Amphipathic Peptides NUMBER OF SEQUENCES: 54
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                                        NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                  ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
US-08-944-133-7
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Pred. No. 0.0029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/232,525
FILLING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: RUMBER: John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

COUNTRY: USA

ID: 70821-2471

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC COMPATIBLE
COMPUTER: PATENTIAN PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DOS/MS-DOS
SOFTWARE: PATENTIAN NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION NUMBER: US/08/944,133
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE: US/08/681,075
FILING DATE: US/08/681,075
FILING DATE: US/08/681,075
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: McLaughlin, Mark L
APPLICANT: McLaughlin, Mark L
APPLICANT: McLaughlin, L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                        RESULT 2
US-08-944-133-3
Sequence 3, Application US/08944133
Patent No. 5789542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McLaughlin, Mark L
                     Best Local Similarity 100.0%;
Matches 14; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                 1 KLAKLAKKLAKLAK 14
                                                                                                         1 KLAKLAKKLAKLAK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-944-133-3
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                                                                                                           PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE: 22-APR-1994
ATORNEY/AGENT INFORMATION:
NAME: RUNNELS, JOHN H
REGISTRATION NUMBER: 33451
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
TELEFAX: 504 346-8049
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-0CT-1997
CLASSIFICATION: 5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIF: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-944-133-26

US-08-944-133-26

Sequence 26, Application US/08944133

Patent No. 5789542

GENERAL INFORMATION:

APPLICANT: McLaughlin, Mark L.

APPLICANT: McLaughlin, Mark L.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: John H. Runnels

STREET: P. O. Box 2471

CITY: Baton Rouge

STATE: LA
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Gaps
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ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DARA:
APPLICATION NUMBER: US/08/944,133
FILING DATE:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-78-1997
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-78-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE: US/08/681,075
FILING DATE: US/08/681,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08944133;
Patent No. 5789542;
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L.
APPLICANT: Becker, Calvin L.
TITLE OF INVENTION: Amphipathic Peptides
CORRESPONDENCE S: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
COTTY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: At
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
504 387-3221
                     TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.

Matches 14; Conservative
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                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-944-133-4
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                                                                                                                                          linear
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                                                                                                                                            TOPOLOGY:
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                                                                                                                                                       APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
INFORMATION FOR SEQ ID No. 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/POCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 70821-2411
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-0CT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 62; DB 1;
; Pred. No. 0.0042;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TILE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
ETLING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
  US/08/944,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-944-133-4
Sequence 4, Application US/08944133
Patent No. 5789542
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
               CLASSIFICATION: 5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-08-944-133-26
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  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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STATE: LA
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Sequence 27, Application US/08723306
Patent No. 3856178
GENERAL INFORMATION:
APPLICANT: White PhD, Kenneth
APPLICANT: Morrey PhD, John
APPLICANT: Correy PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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SOFTWARE:

PATEMITING SISTEM:

APPLICATION NUMBER: US/08/944,133
FILING DATE:

PRICE DATE:

PRICE DATE:

PRICE DATE:

PRICE DATE:

PRICE DATE:

PRICE DATE:

APPLICATION NUMBER: US/08/681,075
FILING DATE:

APPLICATION NUMBER: US/08/681,075
FILING DATE:

APPLICATION NUMBER: US/08/681,075
FILING DATE:

APPLICATION NUMBER: US/08/232,525
FILING DATE:

APPLICATION NUMBER: US/08/232,525
FILING DATE:

APPLICATION NUMBER: 33451

REGISTRATION NUMBER: 33451

REFERENCE/POCKET NUMBER: 33451

REFERENCE/POCKET NUMBER: 346-8049

INFORMATION FOR SEQ 1D NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.9%; Score 57; DB 1; Length 14; 100.0%; Pred. No. 0.014; Live 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Trask Britt and Rossa STREET: P.O. Box 2550 CITY: Salt Lake City CITY: Utah COUNTRY: USA 21P: 84110
                                                                                                      COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 91.9
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Baton Rouge
STATE: LA
CONTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-0CT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                  Sequence 27, Application US/08944133
Patent No. 5785942
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: SAmphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ohn H. Runnels
STREET: P. O. Box 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-944-133-25
Sequence 25, Application US/08944133
Patent No. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION:
TITLE OF INVENTION:
Applipathic Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-944-133-27
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                    1 KLAKLAKKLAKLAK 14
                                          1 KLAKLAKKLAKLAK 14
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Best Local Similarity
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Gaps

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APPLICATION NUMBER: US/08/723,306

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Gaps
                                            Gaps
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GENERAL INFORMATION:
APPLICANT: White PhD, Kenneth
APPLICANT: Reed, William
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask Britt and Rossa
STREET: P.O. Box 2550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application PC/TUS9610041
GENERAL INFORMATION:
APPLICANT: White PhD, Kenneth
APPLICANT: Morrey PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
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  Length 23;
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                                          1; Indels
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MEDIUW TYPE: Floppy disk
COMPUTER: Elboppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10041
FILING DATE:
FLING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SWeigert Plb, Susan E
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
Score 57; DB 2;
Pred. No. 0.022;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
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Pred. No. 0.022;
0; Mismatches
                                      0;
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91.9%;
ilarity 92.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 8015319168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box 2550
CITY: Salt Lake City
STATE: Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 KLKKLAKKLAKLAK 21
                                                                                 1 KLAKLAKKLAKLAK 14
                                                                                                      8 KLKKLAKKLAKLAK 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
  Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                        PCT-US96-10041-27
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APPLICANT: Worrey PhD, John
APPLICANT: Morrey PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammallan Transgenic Organisms
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Trask Britt and Rossa
STREET: P.O. Box 2550
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                          Score 57; DB 2; Length 23;
Pred. No. 0.022;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
            ATTORNEY/AGENT INFORMATION:
NAME: SWeigert PhD, Susan E
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Application US/08723306 Patent No. 5856178 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 8015321922
TELEPAX: 8015319168
INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            91.9%;
92.9%;
                                                                                                                                                                                                                                                                    not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
                                                                                                                                                                                                                                                                    ; TOPOLOGY: not relevar
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-723-306-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. BOX CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide;
HYPOTHETICAL: YES
US-08-723-306-28
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REKKLAKKLAKLAK 21
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Matches 13; Conserv
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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STATE: Ut
COUNTRY:
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US-08-723-306-28
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APPLICANT: Baker, Margaret A.
APPLICANT: Baker, Leonard S.
APPLICANT: Maloy, W. Lee
TITLE OF INVENTION: Treatment of Gynecological
TITLE OF INVENTION: Malignancies with
TITLE OF INVENTION: Biologically Active Peptides
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 1;
Pred. No. 0.053;
4; Mismatches
    PILLING DATE: 15-APR-1991
APPLICATION NUMBER: US 07476629
FILING DATE: 08-FEB-1990
ATTONEY/ABGNT INFORMATION:
NAME: O1Stein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 421250-122
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-994-1740
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:

OTHER INFORMATION: amide-terminated

US-07-908-455A-62
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REGISTRATION NUMBER: 24,025
REFERENCE/DOOKET NUMBER: 421250-194
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/297,950
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/226,108
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  US 07686115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-434-120-88
; Sequence 88, Application US/08434120
; Patent No. 5635479
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.1%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.1
Best Local Similarity 71.4
Matches 10; Conservative
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5 KIAKIAKKIAKIAK 18
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APPLICATION NUMBER:
FILING DATE:
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  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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Sequence 62, Application US/07908455A

Sequence 62, Application US/07908455A

Patent No. 5459237

GENERAL INFORMATION:

APPLICANT: Berkowitz, Barry A.

APPLICANT: Maloy, W. Lee

TITLE OF INVENTION: No. 5459237el Peptide Compositions and TITLE OF INVENTION: No. 5459237el Peptide Compositions and TITLE OF INVENTION: Seg Therefor NUMBER OF SEQUENCES. 89

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carculla, Byrne, Bain, Gilfillan,

STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                            ZIP: 84110

ZIP: 84110

COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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MEDIUM TYPE: 3 5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,455A
FILING DATE: 19920702
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US96/10041 FILING DATE:
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask Britt and Rossa
STREET: P.O. BOX 2550
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SWEIGHT PhD, SUSAN E
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 8015319128
TELEPHONE: 8015319168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 8015319168
INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 23 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 92.9
Matches 13; Conservative
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
PCT-US96-10041-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Roseland
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                          Utah
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                                                                                                                               COUNTRY:
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Gaps

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Gaps
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Pred. No. 0.053;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Magainin Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: 5110 Campus Drive
APPLICANT: 91 Pymouth Meeting, PA 19462
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner CITRET: 1300 I. Street, N.W. Suite 700 STRATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20007-3315
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: 05-JUN-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT IRFORMATION:
NAME: FOTGLS, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0021-03000
TELECOMMUNICATION INFORMATION:
TELECHANE: (202) 408-4400
INDORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86, Application US/08465325 Patent No. 5686563 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Ouery Match 87.1%;
Best Local Similarity 71.4%;
Matches 10; Conservative
201-994-1700
                       TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 21 amino acids
                    201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-434-120-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-325-86
                                                                                                                                                                                                                                                                                                                                                      1 KLAKLAKKLAKLAK 14
|:||:||:||:||
5 KIAKIAKIAKIAK 18
                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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20005-3315
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-465-325-86
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87.1%; Score 54; DB 1; Length 21;

Query Match

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Gaps
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Best Local Similarity 71.4%; Pred. No. 0.053;
Matches 10; Conservative 4; Mismatches 0; Indels
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5 KIAKIAKKIAKIAK 18
                                                  1 KLAKLAKKLAKLAK 14
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                                                                                  Db
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Search completed: May 8, 2002, 07:19:01 Job time: 69 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

May 8, 2002, 07:17:47 ; Search time 38.66 Seconds (without alignments) 26.824 Million cell updates/sec Run on:

US-09-765-086-200 . 62 1 KLAKLAKKLAKLAK 14 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

522463 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

/SIDS8/gcgdata/geneseq/geneseqp/AA1980. /SIDS8/gcgdata/geneseq/geneseqp/AA1981. A_Geneseq_1101:* ••

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/SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

SUMMARIES

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100.0 | Match Length DB 100.0 14 21 19 100.0 21 11 19 100.0 21 11 19 100.0 21 11 19 | DB 19 | H I | Description Minimalist lytic p Antimicrobial pro- Synthetic anti-mic Lytic peptide with Minimalist lytic p |
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AAR07741
AAB21938 | AAB21940
AAE06517 | AAB21937 | AAE00310
AAW62943 | AAW62923 | AAW6292/ | -AAM62941
AAR07743 | AAR13821 | AAR45107 | AAR36366 | AAR31139 | AAR35357 | AAR39069 | AAR55963 | AAR50423 | AAR50539 | AAR56924 | AAR59041 | AAR90129 | AAR83902 | AAY10725 | AAR84167 | AAR77081 | AAR92416 | AAR89973 | AAR07737 | AAR45051 | AAR45108 |
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ALIGNMENTS

AAW62925 standard; peptide; 14 AA (first entry) Minimalist lytic peptide. 02-OCT-1998 AAW62925; ~ AAW62925 RESULT EXXEX DX XXX

Lytic peptide; channel forming peptide; antibacterial; amphipathic. Synthetic

94US-0232525. 96US-0681075. 97US-0789077. 97US-0944133. 97US-0944133 22-APR-1994; 22-JUL-1996; 03-FEB-1997; 06-OCT-1997; 06-OCT-1997; US5789542-A 04 - AUG - 19

(LOUU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.

McLaughlin ML; Becker CL, WPI; 1998-446183/38.

Selective lysis of bacteria amongst mammalian cells – using 14-mer or 21-mer lytic peptides

Gaps

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Indels

Length 14;

100.0%; Score 62; DB 21; 100.0%; Pred. No. 0.0029;

0; Mismatches

14

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useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such antimicrobial peptide, which can be conjugated to a homing peptide to make the homing pro-apoptotic conjugates of the present invention. The present sequence has an amphipathic alpha-helical structure.
                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                       charged amino acid residues, or five nonpolar amino acid residues and two positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues and the positively charged amino acid residues are distributed within the hepted such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha-helix, whereby the multimer is amphipathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                               AAW62920-67 represent minimalist lytic (channel forming) peptides. The peptides have antibacterial properties in concentrations not lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breast; prostate; melanoma; cancer; Kaposl's sarcoma; amphipathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
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                                                                                                                                                                                                                                                           Length 14;
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                                                                                                                                                                                                                                                           100.0%; Score 62; DB 19; 100.0%; Pred. No. 0.0029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial pro-apoptotic peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 104; 118pp; English.
 Claim 3; Column 35; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB21900 standard; Peptide; 14 AA
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Matches
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                                                                                                                                                                                                                                                                   Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;
                                                                                                                                                                                                                                                                                               antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a synthetic anti-microbial peptide having an amphipathic-alpha helical structure. This peptide is linked to a prostate-homing peptide to generate a chimeric prostate-homing pro-apoptotic peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel chimeric prostate-homing pro-apoptotic peptide, used to trea prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
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                                                                                                                                                                                                     Synthetic anti-microbial peptide #1.
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AAE06478 standard; peptide; 14
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22-JUL-1996;
03-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                                                                                                                                                                                                                                                                                   Lysis; neoplastic cells; microbial infections; HIV; P.falciparum; wound healing; adjuvant; hBFSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New lytic polypeptide(s) with proliferative activity - are alpha-helical peptide(s) having aligned amphipathy for treating microbial infections and lysing cancer cells
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Best Local Similarity
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AAW62920-67 represent minimalist lytic (channel forming) peptides. The peptides have antibacterial properties in concentrations not lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively charged amino acid residues. The nonpolar amino acid residues and three positively the positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues and the positively charged amino acid residues and the heptad such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha-helix, whereby the multimer is amphipathic.
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                                                                                                                                                                                                                                                                                                                                                                                         Selective lysis of bacteria amongst mammalian cells – using 14-mer or 21-mer lytic peptides
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96US-0681075.
97US-0789077.
97US-0944133.
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97US-0944133.
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97US-0944133
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Best Local Similarity
Matches 14; Conserv
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WO200042973-A2.
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                                                                                                        Sequence
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AAB21936
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                                                                                                             AAW62920-67 represent minimalist lytic (channel forming) peptides. The peptides have antibacterial properties in concentrations not lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively charged amino acid residues. The nonpolar amino acid residues and three positively the positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues and the positively charged amino acid residues are distributed within the heptad such that when the multimer forms an alpha-helix the anoppolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha-helix, whereby the multimer is amphipathic.
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peptides have antibacterial properties in concentrations not lethal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                             Selective lysis of bacteria amongst mammalian cells – using 14-mer or 21-mer lytic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - using 14-mer
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                                                                                                                                                                                                                                                                            Length 21;
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Pred. No. 0.0042;
Mismatches 0; Indels
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(LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
                                                                                            Disclosure; Column 5; 25pp; English.
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1 Similarity 100.0%;
14; Conservative 0;
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96US-0681075.
97US-0789077.
97US-0944133.
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                      McLaughlin ML;
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                                                                                                                                                                                                                                                                                                                     1 KLAKLAKKLAKLAK
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                                         WPI; 1998-446183/38
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                             21 AA;
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03-FEB-1997;
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                      Becker CL,
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toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively charged amino acid residues. The nonpolar amino acid residues and two positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues are distributed within the heptad such that when the miliner forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha helix, whereby the multimer is amphipathic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 62; DB 19; Length 21; 100.0%; Pred. No. 0.0042;
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8..21
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Matches 14; Conservative
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Chimeric - Unidentified
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Misc-difference
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AAE06512 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                   Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic;
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                                                                    Query Match 100.0%; Score 62; DB 21; Length 21; Best Local Similarity 100.0%; Pred. No. 0.0042; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                        Homing antimicrobial pro-apoptotic conjugate #3.
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homing pro-apoptotic conjugate
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Chimeric - Unidentified.
                                                                                                                               1 KLAKLAKKLAKLAK 14
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                                                                                                                                                                                                                                                                                                                                                                                   alpha-helix; human.
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                            21 AA;
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                                                   Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule; cytostatic; HPP-1.
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/label= Membrane_disrupting_domain
/label= Membrane_disrupting; This region forms an
mphipathic helix and is useful in imparting increased
stability of the conjugate in vivo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, to a patient with prostate cancer. The present sequence is chimeric prostate-homing pro-apoptotic peptide, HPP-1.
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100.0%; Pred. No. 0.0042;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                               /label= Coupling_domain
/note= "Glycinylglycine bridge"
Prostate-homing pro-apoptotic peptide, HPP-1.
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                                                                                                                                                                                                                                                                  1..5
/label= Homing_domain
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Best Local Similarity 100.

Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153342-A1
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                                                                                                                                                                             Jnidentified
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Gaps

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100.0%; Score 62; DB 21; Length 21; 100.0%; Pred. No. 0.0042; Ive 0; Mismatches 0; Indels

14; Conservative

Query Match Best Local Similarity Matches 14; Conserva

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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arap W, Bredesen DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Coupling_domain
/note= "Glycinylglycine bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8..21
/label= Antimicrobial_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- Homing_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 80; 176pp; English.
                                                            AAE06515 standard; peptide; 21 AA.
                                                                                                                                                                                                                                       Homing pro-apoptotic peptide #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2001; 2001WO-US01362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000; 2000US-0489582.
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200153342-A1
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                                                                                                                                                                                                                                                                                                                                                                                                               Jnidentified
                                                                                                                                                                              25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                         cytostatic.
                                                                                                                     AAE06515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
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      RESULT 12
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                                                                                                                        NAME OF THE PROOF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a homing pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses novel chimeric prostate-homing pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ellerby HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3..21
/label= Antimicrobial_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Homing_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Socation/Qualifiers
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                                                                                                                                                                                                      AAE06514 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                    Homing pro-apoptotic peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruoslahti EI, Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-2001; 2001WO-US01362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2000; 2000US-0489582
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                                 1 KLAKLAKKLAKLAK 14
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                           25-SEP-2001
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Key Domain Domain

Domain

Ellerby HM;

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The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a homing proapptotic peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 62; DB 22, 100.0%; Pred. No. 0.0042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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23 AA;
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                                22-JAN-1999;
27-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic.
                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                    This peptide is an analogue of a known lytic peptide. It comprises an alpha helical conformation of amino acids. It is effective at lysing e.g. gram-positive and -negative bacteria and mammalian neoplastic cells, cells infected with intracellular pathogenic microorganisms such as HIV. It stimulates the proliferation of fibroblasts and lymphocytes and can be used in wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.
                                       Lysis; neoplastic cells; microbial infections; HIV; P.falciparum; wound healing; adjuvant; hBFSP.
                                                                                                                                                                                                   New lytic polypeptide(s) with proliferative activity - are alpha-helical peptide(s) having aligned amphipathy for treating microbial infections and lysing cancer cells
                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prostate homing antimicrobial pro-apoptotic conjugate.
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Misc-difference 10..23
/note= "preferably D-form residues"
                       Lytic peptide with proliferative activly.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB21938 standard; Peptide; 23 AA.
                                                                                                                                                                                                                                     Claim 17; page 41; 57pp; English
                                                                                                                                                  (LOUU ) LOUISIANA STATE UNIV
                                                                                                                 90WO-US01945
                                                                                                                                 89US-0336181
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric - Homo sapiens.
Chimeric - Unidentified.
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       22-FEB-1991
                                                                                                                  10-APR-1990;
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                                                                                 409012866-A.
                                                                                                  01-NOV-1990.
                                                                 synthetic.
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                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma breast and prostate cancer or melanoma. The present sequence is one such prostate homing pro-apoptotic conjugate.
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                                                                                                                                                                                                                                                                                                                                    Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to homing pro-apoptotic conjugates
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                                                                                                                                                                                                        Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Glycinyiglycine bridge"
10..23
/label= Antimicrobial_peptide
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                                                                                                                                                                                                        Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Coupling_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 29; Page 108; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE06513 standard; peptide; 23 AA.
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21-JAN-2000; 2000WO-US01602.
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                                                                                                                                                                                                        Ellerby HM, Bredesen DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                      (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                      WPI; 2000-499174/44.
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The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a chimeric prostate-homing pro-apoptotic peptide.
                                                                                                                                                        Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
                                                                                 Ellerby HM;
                                                                                 Bredesen DE,
                                                                                 Arap W,
                                                                                                                                                                                                                                       Claim 6; Page 103; 176pp; English.
                                                                             Ruoslahti EI, Pasqualini R,
21-JAN-2000; 2000US-0489582.
                                          (BURN-) BURNHAM INST.
                                                                                                                   WPI; 2001-451901/48
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Gaps

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Length 23;

Query Match 100.0%; Score 62; DB 22; Length 2 Best Local Similarity 100.0%; Pred. No. 0.0046; Matches 14; Conservative 0; Mismatches 0; Indels

Search completed: May 8, 2002, 07:18:34 Job time: 47 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model
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8, 2002, 07:19:01; Search time 20.74 Seconds (without alignments) 7.595 Million cell updates/sec Run on:

US-09-765-086-207 30 1 SMSIARL 7 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

212252 seqs, 22503292 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database

1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/pCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/pCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | | | , | ١ | | | | | | | | | | | | | | | | | | | | | | | | |
|-----------|--------|-------------|-------------------|------------------|------------------|------------------|-----------------|-----------------|-----------------|-----------------|------------------|-----------------|-----------|-------------------|--------------------|-------------------|-------------------|-------------------|------------------|------|-------------------|------------------|------------------|-------------------|------------------|------------------|------------------|-------------------|------------------|
| | 1 | Description | Sequence 21, Appl | 21, | 5, 4 | 13, | 2, 1 | 7 | 7 | 7 | 68, | 7 | . 54 | Sequence 72, Appl | Patent No. 5175383 | Sequence 1, Appli | 13, | 15, | 10, | 12, | 10, | 13, | ò | Sequence 26, Appl | 12, | 13, | 13, | 13, | 10, |
| SUMMAKIES | | ID | US-09-258-754-21 | US-09-042-107-21 | US-09-045-764A-5 | US-09-413-814-13 | US-08-850-880-2 | US-08-944-916-2 | US-08-814-877-2 | US-08-180-371-2 | US-09-413-814-68 | US-08-102-691-2 | 5430019-2 | US-09-248-335-72 | 5175383-6 | US-08-102-691-1 | US-08-439-725A-13 | US-08-464-590A-15 | US-08-441-629-10 | 7 | US-08-207-412B-10 | US-08-867-471-13 | US-08-438-439C-9 | US-08-951-822-26 | US-09-103-079-12 | US-08-705-245-13 | US-08-718-904-13 | US-09-023-082A-13 | US-08-776-207-10 |
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| | | Length DB | 7 | 7 | 1118 | 439 | 476 | 476 | 476 | 554 | 700 | 175 | 177 | 200 | 205 | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 |
| • | • C | | 100.0 | 100.0 | -7.97 | 76.7 | 76.7 | 76.7 | 76.7 | 76.7 | 76.7 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 |
| | | Score | le
E |)
30 | ,23- | 23 | 23 | 23 | 23 | 23 | 23 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 |
| | Poen1+ | NO. | 1 | 7 | e | ₹ | S | 9 | 7 | 80 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |

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Gaps

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100.0%; Score 30; DB 4; Length 7; 100.0%; Pred. No. 1.6e+05; Live 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 7; Conservative

δŽ g RESULT 2 US-09-042-107-21

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-21

ORGANISM: Artificial Sequence

FEATURE:

Squence 21, Application US/09042107

Batent No. 623287

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosalahti, Erkki
APPLICANT: Rosalahti, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REFERENCE: P-LJ 2892
CURRENT APPLICATION NUMBER: US/09/042,107
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 436
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21

1

| 22 73.3 206
22 73.3 206
22 73.3 331
22 73.3 335
22 73.3 497
22 73.3 497 | 22 73.3 497 4 US-09-118-317-2 Sequence 2, 22 73.3 591 2 US-08-468-249A-20 Sequence 2, 22 73.3 591 2 US-08-468-249A-20 Sequence 20, 22 73.3 1031 3 US-08-313-200-1 Sequence 1, 22 73.3 1091 3 US-08-986-485-5 Sequence 1, 22 73.3 1423 4 US-08-986-485-5 Sequence 1, 22 73.3 4544 2 US-08-865-5 Sequence 52, 22 73.3 4544 2 US-08-469-486-52 Sequence 52, 21 70.0 14 4 US-09-041-886-49 Sequence 55, 21 70.0 14 4 US-09-041-886-55 | 258-754
ence 21
nt No.
ILCANT:
LICANT:
LICANT:
LIC OF I
LE OF I
LE OF I
RENT PI
RENT P | |
|--|---|---|-------------|
| 28
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34 | | RESULT US-09-258-754 Sequence 21, Sequence 21, Batent No. GENERAL INFO APPLICANT: APPLICANT: APPLICANT: TITLE OF II FITLE OF III FITLE APPLIER APP FITLER APP FITLE APPLIER FITLE FITLE | SEQ ID NO 2 |

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Bloecker,
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260 SLSIGRL 266
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STATE: WI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 439
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US-08-850-880-2
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                           ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Synthetic
0S-09-042-107-21
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                                                                                                                                  100.0%; Score 30; DB 4; Length 7; 100.0%; Pred. No. 1.6e+05;
                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94010
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,764A
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                               Sequence 5. Application US/09045764A
Patent No. 6127178
GENERAL INFORMATION:
APPLICANT: Florio, Monica
TITLE OF INVENTION: Apoptotic Peptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UCSF98-045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36.627
REFERENCE/DOCKET NUMBER: UCSF'
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 343-4341
TELEFAX: (650) 343-4341
INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.7
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 75 DENISE DE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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24 SLSIAR 29
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LENGTH: 7
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APPLICANT: Mueller, Joachim
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DN sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Gesellschaft fuer Biotechnologische Forschung mbH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 4; Length 439;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Rezanikoff, William S
APPLICANT: Gorysin, Igor Y
APPLICANT: Zhou, Hong
APPLICANT: Zhou, Hong
TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                         Bristol-Myers Squibb, Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08850880 Patent No. 5925545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960:
TELECOMMUNICATION INFORMATION:
TELECHONE: 608/251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
COGANISM: Sorangium cellulosum
US-09-413-814-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.78;
71.48;
                                                                                           APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.*.
                                                                         Helmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608-251-9166
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                                                                                      Score 23; DB 2; Length 476;
Pred. No. 3.8e+02;
1; Mismatches 0; Indels
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Pred. No. 3.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08944916
Patent No. 5948622
GENERAL INFORMATION:
APPLICANT: Reznikoff, William S
APPLICANT: York, Dona L
APPLICANT: York, Dona L
APPLICANT: Zhou, Hong
TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REPERENCE/DOCKET NUMBER: 960296.94916
TELECOMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/814,877
FILING DATE: 09-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/850,880
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                        76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.7%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                        Query Match 76.7
Best Local Similarity 83.3
Matches 5; Conservative
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               , MOLECULE TYPE: protein US-08-850-880-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-944-916-2
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GY: linear
TOPOLOGY: linear
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427 MAIARL 432
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427 MAIARL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                               2 MSIARL 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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RESULT

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Lymphocytes and Methods of Use Therefor
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                                        GENERAL INFORMATION:
APPLICANT: Goryshin, Igor Y
APPLICANT: Reznikoff, William S
TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB 2; Length 476
Pred. No. 3.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Choudhury, Chandra
TITLE OF INVENTION: Hematopoietic Growth Factor Derived
TITLE OF INVENTION: Hematopoietic Growth Factor Derived
TITLE OF INVENTION: from T
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  960296.94142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08180371
Patent No. 6254861
Sequence 2, Application US/08814877
Patent No. 5965443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/POCKET NUMBER: 9607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.7
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-814-877-2
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| 427 MAIARL 432
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US-08-180-371-2
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21 ALSLARL 27
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5430019-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION;
GENERAL INFORMATION;
GENERAL INFORMATION;
GENERAL INFORMATION;
APPLICANT: Breatlschaft fuer Biotechnologische Forschung mbH
APPLICANT: Beger, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Cino, Paul M
APPLICANT: Cino, Paul M
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: Heteropolyketide compounds
TITLE OF INVENTION: NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER FILING DATE: 1999-10-07
SOFTWARE OF SEQ ID NOS: 107
SOFTWARE PATENTIN VOR: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 4; 1
Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
FILING DATE: 12-JAN-1994
CLASSIFICATION: 424
PURDR APPLICATION DATA:
APPLICATION NUMBER: US 906866
FILING DATE: U1 July 1992
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 27620/31668
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 554 antho acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 68, Application US/09413814; Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Sorangium cellulosum US-09-413-814-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.7
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-180-371-2
                                                                                                                                                                                                                                                                                                                                                                             linear
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358 SISMARL 364
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LENGTH: 700
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RESULT

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5430019-2
; Patent No. 5430019
; Patent No. 5430019
; Patent No. Farent No. 5430019
; TILLE OF INVENTION: HOWGENEOUS K-FGF AND USE OF THE SAME
; TILLE OF INVENTION: HOWGENEOUS K-FGF AND USE OF THE SAME
; UCRRENT APPLICATION DATA:
; APPLICATION UNMBER: US/07/898,051
; FILING DATE: 12-019-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 438,278
; FILING DATE: 16-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
Sequence 2, Application 08/102691
Fatent No. 5559093
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YOSHTONI, Sumie
APPLICANT: GGRAGHI, Koichi
TILE OF INVENTION: PLATELET-INCREASING AGENT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS 6
STREET: 100 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.3%; Score 22; DB 6; Length 177; Best Local Similarity 57.1%; Pred. No. 2.2e+02; Matches 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 175;
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Pred. No. 2.2e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGFWARE: Patentin Release #1.0, Version #1.25
SUFWARE: Patentin Release #1.0, Version #1.25
SUFWARE: PATENTIN DATE:
APPLICATION NUMBER: 08/102,691
FILING DATE:
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION NUMBER: 3628
REFERENCE/DOCKET NUMBER: 42835
TELEPHONE: (617)523-6440
TELEPHONE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 175 amino acids
amino acid
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Best Local Similarity 57.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
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TYPE: amino acid
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52 ALSLARL 58
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                                   COUNTRY:
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STATE:
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5175383-6
; Patent No. 5175383
APPLICANT: LEDER, PHILIP; MULLER, WILLIAM J.
TITLE OF INVENTION: ANIMAL MODEL FOR BENIGN PROSTATIC DISEASE
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: OCCUPION:
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION:
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT APPLICATION NUMBER: US/09/24,759
EARLIER RELIGNE DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 72
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-102-691-1

Sequence 1, Application 08/102691
Sequence 1, Application 08/102691
GENERAL INFORMATION:
APPLICANT: KUROKAWA, TSULOMU
APPLICANT: IGARASHI, Koichi
TITLE OF INVENTION: PLATELET-INCREASING AGENT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS 6
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 73.3%; Score 22; DB 6; Length 205; Similarity 57.1%; Pred. No. 2.6e+02; 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 3; Length 200
Pred. No. 2.5e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/312,641
FILING DATE: 17-FEB-1989
                                                                                                                    Sequence 72, Application US/09248335 Patent No. 6096504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.3%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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52 ALSLARL 58
                 ::|:|||
23 ALSLARL 29
1 SMSIARL 7
                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: maize US-09-248-335-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SMSIARL 7
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; LENGTH: 205
                                                                                                  US-09-248-335-72
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                     ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Gaps
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APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
CORRESPONDENCE: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/102,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22; DB 1; Le
Pred. No. 2.6e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/047001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,725A
FILIGO DATE: 12-MAY-1995
CLASSIFICATION: 424
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/08439725A Patent No. 5693775 GENERAL INFORMATION:
                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEEN, Ronald I
REGISTRATION NUMBER: 30628
REFRENCE/CDOCKET NUMBER: 4283
TELEPRONE: (617)523-3400
TELEPAX: (617)523-3400
TELEFAX: (617)523-3400
TELERAX: (617)523-3400
TELEFAX: (617)523-3400
TELEFAX: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-102-691-1
Massachusetts
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: INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-439-725A-13
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0; 0; Gaps Query Match 73.3%; Score 22; DB 1; Length 206; Best Local Similarity 57.1%; Pred. No. 2.6e+02; Matches 4; Conservative 3; Mismatches 0; Indels

1 SMSIARL 7 ::|:||| 52 ALSLARL 58 δλ

Op

Search completed: May 8, 2002, 07:19:02 Job time: 70 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

May 8, 2002, 13:31:42; Search time 23.87 Seconds Run on:

(without alignments)
71.374 Million cell updates/sec

CHIMERA Title: Perfect score:

104 1 SMSIARLGGKLAKLAKKLAKLAK Sequence:

23

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

522463 seqs, 74073290 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

| | | | | | SUMMARIES | |
|--------|-------|-------|--------------------|----|-----------|---------------------|
| | | ф | | | | |
| Result | | Query | | | | |
| No. | Score | Match | Match Length DB ID | DB | | Description |
| | 104 | 100.0 | 23 | 21 | AAB21938 | Prostate homing an |
| 7 | 104 | 100.0 | 23 | 22 | AAE06513 | Chimeric prostate |
| m | 78 | 75.0 | 21 | 21 | AAB21936 | Homing antimicrobi |
| 4 | 7.8 | 75.0 | | 22 | AAE06512 | Prostate-homing pr |
| S | 74 | 71.2 | | 21 | AAB21939 | Homing antimicrobi |
| 9 | 74 | 71.2 | 21 | 22 | AAE06514 | Homing pro-apoptot |
| 7 | 74 | 71.2 | | 22 | AAE06515 | Homing pro-apoptot |
| 80 | 74 | 71.2 | 25 | 21 | | Homing antimicrobi |
| 6 | 74 | 71.2 | | 22 | | Homing pro-apoptot |
| 10 | 74 | 71.2 | 26 | 21 | | Homing antimicrobi |
| 11 | 7.4 | 71.2 | 26 | 22 | | Homing pro-apportot |

| 1, 72 69.2 21 19 AAM62926 13 72 69.2 28 19 AAM62923 14 72 69.2 28 19 AAM62923 15 67 64.4 21 19 AAM62925 19 65 59.6 14 19 AAM62925 19 62 59.6 14 21 AAM62925 20 62 59.6 14 21 AAM62925 21 62 59.6 14 22 AAM62925 22 62 59.6 21 14 AAM62925 23 62 59.6 21 14 AAM62925 24 62 59.6 21 14 AAM31081 25 62 59.6 21 14 AAM31081 26 59.6 21 14 AAM31081 27 62 59.6 21 14 AAM31081 28 62 59.6 21 14 AAM31081 29 62 59.6 21 15 AAM55905 29 62 59.6 21 15 AAM59013 29 62 59.6 21 15 AAM59013 29 62 59.6 21 15 AAM59013 29 62 59.6 21 15 AAM59065 31 62 59.6 21 15 AAM59065 32 62 59.6 21 15 AAM59065 33 62 59.6 21 15 AAM59065 34 62 59.6 21 15 AAM59066 35 61 58.7 42 14 AAM39066 36 57.7 21 12 AAM13818 39 60 57.7 21 12 AAM13818 39 60 57.7 21 14 AAM45075 44 60 57.7 21 14 AAM31071 45 60 57.7 21 14 AAM31071 | | list lytic | ist lytic | list lytic | lytic | lytic | Minimalist lytic p | lytic | al pro | Synthetic anti-mic | u | Basic (positively | Amphiphilic ion ch | C-terminal substd. | Amphiphilic peptid | | Ion channel formin | Amphiphillic pepti | Amphiphilic peptid | 1) | Cancer treating, a | (KLAGKLA)3 peptide | Ion channel formin | Peptide used to ma | Φ | Lytic peptide with | Biologically activ | Amphiphilic peptid | PGLa peptide compo | Basic (positively | Basic (positively | | Amphiphilic ion ch | -terminal su | PGLa-derived antim | |
|---|---|------------|-----------|------------|----------|----------|--------------------|----------|----------|--------------------|----------|-------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-----|--------------------|--------------|--------------------|--|
| 72 69 72 72 72 72 72 72 72 72 72 72 72 72 72 | | AAW62926 | AAW62943 | AAW62923 | AAW62927 | AAW62942 | AAW62922 | AAW62925 | AAB21900 | AAE06478 | AAR07747 | AAR45051 | AAR36310 | AAR31081 | AAR35299 | AAR39013 | AAR55905 | AAR50481 | AAR50365 | AAR55620 | AAR58965 | AAR90073 | AAR83844 | AAY10669 | AAR07741 | AAR07743 | 906 | 381 | 999 | 504 | 507 | 530 | 533 | 103 | 911 | |
| 5 4 3 3 5 5 6 6 6 6 5 7 7 7 7 7 7 7 7 7 7 7 7 7 | | 19 | 19 | 13 | 19 | 19 | 13 | 13 | 21 | 22 | 11 | 14 | 14 | 14 | 14 | 14 | 15 | 15 | 15 | 12 | 15 | 16 | 16 | 20 | 11 | 11 | 14 | 12 | 12 | 14 | 14 | 14 | | | 17 | |
| 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | | 21 | 28 | 28 | 28 | 21 | 21 | 14 | 14 | 14 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 23 | 38 | 42 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | |
| | | 6 | 6 | 6 | 6. | 4 | ω. | 6 | 6 | 6 | 6 | ó, | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 6 | 8 | æ | 7 | 7 | 7 | 7 | 7. | 7. | 7 | 7 | |
| , ПППППППСОООООООООООООООООООООООООООООО | | 72 | 72 | 72 | 72 | 67 | 99 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 61 | 61 | 09 | 09 | 09 | 09 | 09 | 09 | 9 | 09 | |
| | , | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | |

ALIGNMENTS

RESULT

AAB21938 standard; Peptide; 23 AA

AAB21938;

22-MAR-2001

Prostate homing antimicrobial pro-apoptotic conjugate. (first entry)

Cytostatic; homing.pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.

Chimeric - Homo sapiens. Chimeric - Unidentified.

Key Location/Qualifiers Misc-difference 10..23 /note= "Preferably D-form residues"

WO200042973-A2

27 - JUL - 20.00.

21-JAN-2000; 2000WO-US01602.

99US-0235902. 22-JAN-1999;

(BURN-) BURNHAM INST

Ruoslahti EI; Pasqualini R, Ellerby HM, Bredesen DE,

WPI; 2000-499174/44.

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The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to anglogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                Homing pro-apoptotic conjugate comprising a tumor homing molecule that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an
                              selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ellerby HM;
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                                                                                                                                                                                                                                                                                                                                                     Length 23;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 104; DB 21;
100.0%; Pred. No. 7.1e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8..9
/label= Coupling_domain
/note= "Glycinylglycine bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric prostate-homing pro-apoptotic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..7
/label= Prostate_homing_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10..23
/label- Antimicrobial_peptide
                                                                                                                                                                                                                                                                          prostate homing pro-apoptotic conjugate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .ocation/Qualifiers
                                                                           Claim 29; Page 108; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SMSIARLGGKLAKLAKKLAKLAK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE06513 standard; peptide; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruoslahti EI, Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-2001; 2001WO-US01362.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-451901/48.
                                                                                                                                                                                                                                                                                                       23 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic.
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prostate cancer, comprantimicrobial peptide

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The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to anglogenic vasculature. The antimicrobial peptide has low mammalian cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                     The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a chimeric prostate-homing pro-apoptotic peptide.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic;
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                             Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Preferably D-form residues"
                                                                                                                                                                                                                                                                            Score 104; DB 22;
Pred. No. 7.1e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homing antimicrobial pro-apoptotic conjugate #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 105; 118pp; English.
             Claim 6; Page 103; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                            100.0%; Some 100.0%; Protive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB21936 standard; Peptide; 21
                                                                                                                                                                                                                                                                                                                                                              21-JAN-2000; 2000WO-US01602.
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                                                                                                                                                                                                                                                                                                              Conservative
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Chimeric - Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-helix; human.
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                               23 AA;
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Gaps

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chimera.rag

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toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such homing pro-apoptotic conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6..21
/label- Membrane_disrupting_domain
/label- Antimicrobial peptide; This region forms an
amphipathic helix and is useful in imparting increased
stability of the conjugate in vivo"
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ellerby
                                                                                                                                        Score 78; DB 21; Length 21;
Pred. No. 4.2e-05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Glycinylglycine bridge"
                                                                                                                                                                                                                                                                                                                                                                                                          Prostate-homing pro-apoptotic peptide, HPP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Coupling_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label~ Homing_domain
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                                                                                                                                                                                                                                                                                                                 AA.
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0
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                                                                                                                                        75.0%;
94.4%;
                                                                                                                                                                                                                                                                                                              AAE06512 standard; peptide;
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                                                                                                                                                                                                      6 RLGGKLAKLAKKLAK 23
                                                                                                                                                                                                                      4 rcggklaklakklaklak 21
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                       Conservative
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                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; HPP-1.
                                                                                           21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                             AAE06512;
                                                                                                                                          Query Match
                                                                                                                                                        Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such homing pro-apoptotic conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer-
to direct an antimicrobial peptide in vivo to a prostate cancer, to induce salective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is chimeric prostate-homing pro-apoptotic peptide, HPP-1.
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposl's sarcoma; amphipathic; alpha-helix; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to homing pro-apoptotic conjugates,
                                                                                                                                                        ö
                                                                                                                          Length 21;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8..21
/note= "Preferably D-form residues"
                                                                                                                                                                                                                                                                                                                                                                                             Homing antimicrobial pro-apoptotic conjugate #3.
                                                                                                                         Score 78; DB 22;
Pred. No. 4.2e-05;
                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 8; 118pp; English.
                                                                                                                                                                                                                                                                                                   AAB21939 standard; Peptide; 21 AA.
                                                                                                                         75.0%;
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                                                                                                                                                                                       6 RLGGKLAKLAKLAK 23
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                                                                                                                                         Best Local Similarity 94.4 Matches 17; Conservative
                                                                                                                                                                                                      - Homo sapiens
- Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bredesen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-499174/44.
                                                                           21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200042973-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ellerby HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric Chimeric
                                                                              Sequence
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                  AAB21939;
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(first entry)

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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                                                                                                                                                             Homing pro-apoptotic peptide #2.
                                                                              AAE06515 standard; peptide;
 6 ggklaklakklaklak 21
                                                                                                                                                                                                                                         Unidentified
                                                                                                                                  25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                                               cytostatic.
                                                                                                         AAE06515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                    Key
Domain
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Matches
                                                     RESULT
                                                                   AAE065
               셤
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                                                                                                                                                                                                                                                     Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a homing pro-
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel chimeric prostate-homing pro-apoptotic peptide, used to tree prostate cancer, comprises a prostate-homing peptide linked to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HM;
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DB 21; Length 21; 0.00016;
                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bredesen DE,
                                                                                                                                                                                                                                                                                                                                                                                    . Coupling_domain
"Glycinylglycine bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                 8..21
/label= Antimicrobial_peptide
Score 74; DB 2; Pred. No. 0.0000; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   |...5
/label= Homing_domain
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 80; 176pp; English.
                                                                                                                                               AAE06514 standard; peptide; 21 AA.
  71.20,
100.08; Pie
                                                                                                                                                                                                                            Homing pro-apoptotic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       æ
 71.2%;
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                                                                                                                                                                                                 (first entry)
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                          Conservative
                                                                 6 ggklaklakklaklak 21
                                                    8 GGKLAKLAKKLAK 23
                                                                                                                                                                                                                                                                                                                                                                                    /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antimicrobial peptide -
                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BURN-) BURNHAM INST.
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            Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153342-A1
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                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                 25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                               cytostatic
                                                                                                                                                                       AAE06514;
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a homing proapptotic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to trea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses novel chimeric prostate-homing pro-apoptotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                               Ellerby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel chimeric prostate-homing pro-apoptotic peptide, used t
prostate cancer, comprises a prostate-homing peptide linked
antimicrobial peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.2%; Score 74; DB 22; I 100.0%; Pred. No. 0.00016; ive 0; Mismatches 0;
                                                                                  /label= Coupling_domain
/note= "Glycinylglycine bridge"
8..21
/label= Antimicrobial_peptide
                            1..5
/label= Homing_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                  Arap W,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 80; 176pp; English.
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                                                                                                                                                                                                                                                                                             16-JAN-2001; 2001WO-US01362
                                                                                                                                                                                                                                                                                                                                        21-JAN-2000; 2000US-0489582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 GGKLAKLAKKLAKLAK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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nes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                      WO200153342-A1
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Gaps

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71.2%; Score 74; DB 100.0%; Pred. No. 0.0

Query Match 71.2 Best Local Similarity 100. Matches 16; Conservative

8 GGKLAKLAKKLAKLAK 23

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25 AA;
                                                                                                                                                               WO200153342-A1.
                                                                                                                                                                                                                                                                   Ruoslahti EI,
                                                   Jnidentified
                                                                                                                                                                                   26-JUL-2001.
                               cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                       Key
Domain
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                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell excitity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such
                                                                                                                                                                                                                                                                                                                                                Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                        Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.
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/note= "Preferably D-form residues"
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Pred. No. 0.00019;
0; Mismatches 0;
                                                                     Homing antimicrobial pro-apoptotic conjugate #4.
                                                                                                                                                                                                                                                                                                          Pasqualini R,
                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 8; 118pp; English.
         AAB21940 standard; Peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.2%; Scc.
100.0%; Pre
0; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homing pro-apoptotic peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pro-apoptotic conjugate
                                                                                                                                                                                                                                             21-JAN-2000; 2000WO-US01602.
                                                                                                                                                                                                                                                                  99US-0235902.
                                                 (first entry)
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                                                                                                                                                                                                                                                                                                          Bredesen DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.2
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                      (BURN-) BURNHAM INST
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                                                                                                                                                                      Misc-difference 12
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                                                 22-MAR-2001
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                            AAB21940;
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AAB21940
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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.
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100.0%; Pred. No. 0.00019;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          10..11
/label= Coupling_domain
/note= "Glycinylglycine bridge"
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                                                                                                                                                                                                                                                                                                                                                  /note= "Glycinylglycine bridge
12..25
/label= Antimicrobial_peptide
                                                                                                                                                                                                                                 ...9
/label= Homing_domain
                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2001; 2001WO-US01362.
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Matches 16; Conserv
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Domain
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                                                                                                                                                                                                                                                                  The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to ampliogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such homing pro-apoptotic conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule; cytostatic.
                                                                                                                                                                                                          Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74; DB 21; Length 26;
Pred. No. 0.0002;
0; Mismatches 0; Indels
                                                                                                                                                                      Ruoslahti EI;
                         Key Location/Qualifiers
Misc-difference 13..26
/note= "Preferably D-form residues"
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/label= Coupling_domain
/note= "Glycinylglycine bridge"
                                                                                                                                                                      Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Homing_domain
                                                                                                                                                                                                                                                Claim 13; Page 105; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                            71.2%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homing pro-apoptotic peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE06516 standard; peptide; 26
                                                                                                          21-JAN-2000; 2000WO-US01602
                                                                                                                             99US-0235902
                                                                                                                                                                     Ellerby HM, Bredesen DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 GGKLAKLAKKLAK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Homo sapiens
- Unidentified
                                                                                                                                                 (BURN-) BURNHAM INST.
                                                                                                                                                                                       WPI; 2000-499174/44.
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       26 AA;
                                                                   WO200042973-A2
                                                                                                                            22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-2001
                                                                                      27-JUL-2000
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE06516;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Domain
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The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a homing pro-apoptotic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                                                                                                                                                                                                                                                                                Ellerby HM;
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Pred. No. 0.0002;
0; Mismatches 0; Indels
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13..26
/label= Antimicrobial_peptide
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100.08; F1.
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96US-0681075.
97US-0789077.
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimalist lytic peptide.
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                                                                                                                                                                                                                                                                 (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-451901/48.
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                                                                     WO200153342-A1
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.03-FEB-1997;
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Query Match
Best Local Similarity
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                                                                                                                                                peptides have antibacterial properties in concentrations not lethel toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively charged amino acid residues. The nonpolar amino acid residues are not the positively charged amino acid residues. The nonpolar amino acid residues are distributed within the heptad such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha-helix, whereby the multimer is amphipathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW62920-67 represent minimalist lytic (channel forming) peptides. The peptides have antibacterial properties in concentrations not lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                                                                                                   AAW62920-67 represent minimalist lytic (channel forming) peptides.
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                                                         Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-mer lytic peptides
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                                                                                                                                                                                                                                                                                                                                                           69.2%; Score 72; DB 19; Length 21; 80.0%; Pred. No. 0.00032; ive 2; Mismatches 2; Indels
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                                                                                                       Disclosure; Column 5; 25pp; English.
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96US-0681075.
97US-0789077.
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McLaughlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-446183/38.
                            WPI; 1998-446183/38
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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22-JUL-1996;
03-FEB-1997;
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Becker CL,
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charged amino acid residues, or five nonpolar amino acid residues and two positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues are distributed within the heptad such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha-helix,
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80.0%; Pred. No. 0.00042;
Mismatches 2;
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Pred. No. 0.00042;
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80.0%;
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Best Local Similarity
Matches 16; Conserv
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Gaps
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 2; Indels
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 Mismatches
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                                                                                                                                   AAW62927 standard; peptide; 28 AA.
5;
                          94US-0232525.
96US-0681075.
97US-0789077.
97US-0944133.
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16; Conservative
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22-JUL-1996;
03-FEB-1997;
06-OCT-1997;
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                                                                                                       RESULT 15
Matches
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4 IARLGGKLAKLAKKLAKLAK 23 δ g

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Score 72; DB 19; Length 28; Pred. No. 0.00042; 2; Mismatches 2; Indels

69.2%; 80.0%;

Query Match 69.2 Best Local Similarity 80.0 Matches 16; Conservative

8, 2002, 13:34:52 Search completed: May Job time: 190 sec